



**Mechanisms of apoptosis regulation in human cells infected with
Simkania negevensis.**

**Mechanismen der Apoptoseregulation in *Simkania negevensis*
infizierten Humanzellen.**

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Würzburg,

Dedicated to my beloved father

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I. Table of contents	7
II. Figure and Table Index	14
III. Abbreviations	19
IV. Summary	21
V. Zusammenfassung	23
1. Introduction	23
1.1. <i>Chlamydiales</i>	23
1.1.1. History	23
1.1.2. Taxonomy	24
1.1.3. Pathogenicity and epidemiology of <i>Simkania negevensis</i>	27
1.1.4. The Chlamydial life style	28
1.2. Cell death: Evolution	32
1.2.1. Morphological and biochemical features of apoptosis	33
1.2.2. Apoptosis- the fundamental mechanism of PCD	35
1.2.3. Caspases the major classes of apoptosis mediators	36
1.2.4. Consequences of caspase activation	39
1.2.5. Inhibitors of apoptosis (IAPs) the cellular inhibitor of caspases	40
1.2.6. The Bcl-2 family	42
1.2.7. NF-κB, the master regulator	48
1.2.8. The Akt/PKB signaling pathway	52
1.2.9. The extrinsic pathway of apoptosis	53
1.2.10. The intrinsic pathway of apoptosis	57
1.2.11. Perforin/ granzyme B pathway	59
1.3. Manipulation of host cell death pathway during microbial infection	60
1.3.1. Regulation of apoptosis during infection	60
1.3.2. Regulation of necrosis during infection	62
1.3.3. Regulation of pyroptosis during infection	63

1.3.4. Apoptosis and host cell modulation by <i>Chlamydiales</i>	63
1.4. Aim of the work	67
2. Materials and methods	74
2.1. Materials	74
2.1.1. Cell lines	74
2.1.2. Bacterial strain used in the study	74
2.1.3. Amoebal strain used in the study	74
2.1.4. Cell culture	75
2.1.5. Buffer and Solutions	76
2.1.5. i. Buffer for Immunofluorescence	76
2.1.5. ii. Buffer for Immunoblotting	77
2.1.6. Commercial Kits used in the study	78
2.1.7. Inhibitors, Inducers used in the study	78
2.1.8. Fine chemicals used in the study	78
2.1.9. Antibodies used in the study	79
2.1.10. Technical equipment used in the study	79
2.1.11. Software used in the study	79
2.2. Methods	68
2.2.1. Cell culture	76
2.2.1a. Amoebal culture	76
2.2.2. Cryo stocking of cell lines	76
2.2.3. Infection with <i>Simkania negevensis</i>	77
2.2.4. Preparation of bacterial stocks	77
2.2.5. Titration of bacterial stocks	78
2.2.6. Apoptosis induction	78
2.2.7. Assays to measure apoptosis	78
2.2.7.1. Hoechst or DRAQ5 staining	79
2.2.7.2. TUNEL assay	80
2.2.7.3. Luminescent caspases-8 activity assay	81
2.2.7.4. Cytochrome c release	81

2.2.7.5. Active caspase-3 staining	81
2.2.7.6. Activation of Bax	81
2.2.7.7. Heterodimerisation of Bax and Bak	81
2.2.8. Infectivity assays	83
2.2.9. Inhibitor treatment	84
2.2.10. Transfection	84
2.2.10.1. Polyethylenimine (PEI) transfection	85
2.2.10.2. Lipofectamine™ 2000 DNA delivery	85
2.2.11. Microscopy	86
2.2.11.1. Leica Fluorescence microscopy	86
2.2.11.2. Confocal microscopy	86
2.2.11.3. Electron microscopy	86
2.2.12. SDS-PAGE and Western blotting	87
2.2.14. Electro Mobility Shift Assay	89
2.2.15. RNA isolation	90
2.2.16. DNA digestion	90
2.2.17. Copy (c) DNA synthesis	91
2.2.18. qRT PCR	91
2.2.19. Statistical analysis	91
3. Results	92
3.1. Establishing <i>S. negevensis</i> infection in cell cultures	92
3.2. <i>S. negevensis</i> infected cells are resistant to apoptosis induced by TNF- α /chx	94
3.3. Sn infected cells resists apoptosis in a time and MOI dependent manner	96
3.4. Sn infected cells resist apoptosis induced by Staurosporine	99
3.5. TNFR is not in cells shed during Sn infection	100
3.6. Caspase maturation is differentially regulated in <i>Simkania</i> -infected cells	102
3.7. <i>Simkania</i> infection inhibits apoptosis on the upstream of mitochondria	105

3.8. Pro-apoptotic BH3-only proteins are not degraded in <i>Simkania</i> -infected cells	110
3.9. Anti-apoptotic Bcl-2 family members are not regulated in Sn-infected cells	111
3.10. NF- κ B is activated upon Sn infection	112
3.11. NF- κ B inhibition sensitize the Sn-infected cells for apoptosis	116
3.12. NF- κ B inhibitors reduced the infectivity of Sn	118
3.13. Akt is activated in Sn infected cell	120
3.14. Activation of PI3-kinase pathway is required for apoptosis inhibition in Sn-infected cells	121
3.15. cIAPs are up-regulated and required for apoptosis resistance in Sn-infected cells	123
3.16. Sn protects <i>Acanthamoeba Castellanii</i> during starvation	127
4. Discussion	130
4.1. Resistant to apoptosis is highly conserved in the order <i>Chlamydiales</i>	130
4.2. Sn resists apoptosis in infected cells in a time and MOI-dependent manner	132
4.3. Sn infection can resist apoptosis signaling upstream of mitochondria	133
4.4. Caspases are differentially regulated upon Sn infection	136
4.5. Caspase-8 is activated upon Sn infection	138
4.6. Akt is activated upon Sn infection	138
4.7. NF- κ B is activated upon Sn infection	140
5. Outlook	145
6. References	147
7.1. Curriculum vitae	174
7.2. List of publications	177

II. Figure and Table Index

11

Figures

Figure 1.1. The phylogenetic tree of <i>Chlamydiales</i>	25
Figure 1.2. The life cycle of <i>Chlamydiales</i>	30
Figure 1.3. Transmission electron micrograph of <i>Chlamydiales</i>	32
Figure 1.4. Evolutionary comparison of cell death in <i>C. elegans</i> and mammalian cells	36
Figure 1.5. The sketch of three major groups of caspases and its activation	39
Figure 1.6. Molecular sketch of cIAPs	42
Figure 1.7. Molecular sketch of the pro, multi-domain and anti-apoptotic BH3-only proteins	44
Figure 1.8. Mechanism of NF- κ B activation	50
Figure 1.9. Overview of Akt activation and its consequences	53
Figure 1.10. The intrinsic and extrinsic pathway of apoptosis	58
Figure 1.11. Regulation of apoptosis during infection	66
Figure 3.1a. Establishing Sn infection in different cell lines	93
Figure 3.1b. Transmission electron micrograph of Sn in membranous inclusion	93
Figure 3.2a. Immunofluorescence analysis of Sn-infected and apoptosis induced HeLa cells	94
Figure 3.2b. TUNEL assay of Sn-infected apoptosis induced cells	95
Figure 3.2c. Bar diagram displaying the quantitative analysis of apoptosis	96
Figure 3.3a. Immunofluorescence analysis of time and dose dependent assay	97
Figure 3.3b. Quantitative analysis of apoptosis for time dependency of Sn	98
Figure 3.3c. Quantitative analysis of apoptosis for dose dependency of Sn	99
Figure 3.4. Quantitative analysis of an infection/apoptosis induction after TNF- α /STS induction	100
Figure 3.5. TNF receptor is activated in <i>Simkania</i> -infected cells	101
Figure 3.6a. Western blot analysis for PARP and caspase cleavage	102
Figure 3.6b. Immunofluorescence staining of active caspase-3	103

Figure 3.6c. Quantitative analysis of caspase-3 activation	104
Figure 3.6d. Quantitative analysis of caspase-8 activation	105
Figure 3.7a. Immunofluorescence staining of cytochrome c on <i>Simkania</i> infection	107
Figure 3.7b. Immuno-blot analysis cytochrome c in cytoplasmic and mitochondrial fraction on <i>Simkania</i> -infection	108
Figure 3.7c. Heterodimerisation assay for activated Bax and Bak	108
Figure 3.7d. Immunofluorescence staining of active Bax in Sn infected/induced cells	109
Figure 3.8. Immunoblot analysis of the pro-apoptotic BH3-only Bcl-2 family members during <i>Simkania</i> infection	110
Figure 3.9. Western blot analysis of Bcl-2 proteins in Sn infected cells	112
Figure 3.10a. HeLa cells with or without <i>Simkania</i> infection induced with TNF α - without chx	113
Figure 3.10b. Immunofluorescence staining of p65 in Sn infected and uninfected cells	114
Figure 3.10c. EMSA of NF- κ B activation in Sn infected cells	115
Figure 3.11a. Bar diagram showing the percentage of apoptosis after CAPE treatment	116
Figure 3.11b. Immunoblot analysis of PARP cleavage after CAPE sensitization	117
Figure 3.11c. Immunofluorescence of samples treated after CAPE sensitization	117
Figure 3.12a. Bar diagram showing the <i>Simkania</i> infectivity assay	118
Figure 3.12b. Immunofluorescence analysis <i>Simkania</i> infectivity assay	119
Figure 3.13. Immunoblot analysis of the anti-apoptotic/ pro-survival signaling during <i>Simkania</i> infection	120
Figure 3.14a. Immunoblot analysis of apoptosis after Akt inhibitor treatment	122
Figure 3.14b. Bar diagram showing the percentage of apoptosis after Akt inhibitor treatment	122
Figure 3.14c. Immunofluorescence of samples treated after Akt inhibitor treatment	123
Figure 3.15a. Immunoblot analysis of the cIAPs during <i>Simkania</i> infection.	124

Figure 3.15b. RT PCR of different cIAPs during <i>Simkania</i> infection.	125
Figure 3.15c. PARP cleavage showing the sensitization of apoptosis	126
Figure 3.15d. Bar diagram showing percentage of apoptosis after cIAPs KO	127
Figure 3.16. Sn infection protects <i>A. castellanii</i> during starvation	128
Figure 4.17. Overview of the anti-apoptotic mechanism in Sn-infected cells	143

Tables

Table 1.1. List of the different species in the genus <i>Chlamydia</i>	26
Table 1.2. Subfamily of caspases and their function	38
Table 2.1. Human tissue culture cell lines used in the study	68
Table 2.2. Bacterial strains used in the study	68
Table 2.3. List of cell culture medium	70
Table 2.4. Buffers for immunofluorescence	70
Table 2.5. Buffers for immunoblotting	71
Table 2.6. Commercial kits used	72
Table 2.7. Inhibitors and inducers used	72
Table 2.8. List of fine chemicals	72
Table 2.9. List of primary antibodies used	73
Table 2.10. List of secondary antibodies used	74
Table 2.11. Components of SDS-PAGE	87

III. Abbreviations

A

AIF	Apoptosis-inducing factor
Apaf-1	Apoptotic protease activating factor 1
APS	Ammonium per sulfate
ATCC	American Type Culture Collection

B

Bad	Bcl-2 antagonist, causing cell death
Bak	Bcl-2 homologous antagonist killer
Bax	Bcl-associated X protein
Bcl-2	B-cell lymphoma- 2
BH	Bcl-2 homology
Bid	Bcl-2 interacting protein
Bik	Bcl-2 interacting killer
Bim	Bcl-2 interacting mediator of cell death
Bmf	Bcl-2 modifying factor
bps	Base pairs
BSA	Bovine serum albumin

C

CED	Cell Death Abnormal
cFLIP	Cellular FLICE like inhibitory protein
Cpn	<i>Chlamydia pneumonia</i>
Ctr	<i>Chlamydia trachomatis</i>

D

dpi	Days post infection
DED	Death effector domain
DEPC	Diethylpyrocarbonate
DMSO	Dimethyl sulphoxide

E

EB	Elementary body
ECL	Enhanced chemiluminescence
EDTA	Ethylene diamine tetra acetic acid
e.g.	Exempli gratia (for example)
ERK	Extracellular signal regulated kinase

F

FADD	Fas associated death domain
FBS	Fetal bovine serum

H

hpi	Hours post infection
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HIV	Human immunodeficiency virus
HMBG1	High mobility Box group 1
Hsp	Heat Shock Protein

I

IAPs	Inhibitor of apoptosis proteins
IB	Immunoblotting
ICE	Interleukin-1 β -converting enzyme
IL-1	Interleukin 1
i.e.	<i>id est</i> , that is
IF	Immuno fluorescence
IFU	Inclusion forming unit
I κ B	inhibitor of kappa
Ig	Immunoglobulin
IPAF	ICE protease activating factor

K

kDa	Kilo Dalton
-----	-------------

L

l	Liter
---	-------

M

M	Molar
mM	Milli molar
μ M	Micro molar
nM	Nano molar
MAPK	Mitogen activated protein kinase
Mcl-1	Myeloid cell lymphoma-1
MEK	MAP ERK kinase
MOI	Multiplicity of infection
ms	Mouse
MMP	Mitochondria membrane potential
min	Minutes

N

NF- κ B	Nuclear Factor kappa B
----------------	------------------------

P

PARP	Poly ADP ribose polymerase
PBS	Phosphate buffer saline
PCD	Programmed cell death
PCR	Polymerase chain reaction
PFA	Paraformaldehyde
PVDF	Polyvinylidene fluoride

Q

qRT PCR	Quantitative Real Time PCR
---------	----------------------------

R

rb	Rabbit
RB	Reticulate body
RNA	Ribonucleic acid
rpm	Revolutions per minute
RT	Room temperature

S

SD	Standard deviation
----	--------------------

SDS	Sodium dodecyl sulfate
SDS-PAGE	SDS polyacrylamidegel electrophoresis
s	Second
Sn	<i>Simkania negevensis</i>
siRNA	Small interfering RNA
SPG	Sucrose phosphate glutamate
STS	Staurosporine
SSC	Saline sodium citrate
T	
TNF- α	Tumor necrosis factor alpha
tBid	Truncated BID
TBS	Tris buffer saline
TLR	Toll like receptor
TUNEL	Terminal deoxynucleotidyl transferase dUTP nick end labelling
V	
v/v	Volume per volume
W	
w/v	Weight per volume

IV. Summary

Chlamydiales are obligate intracellular gram-negative bacteria that have gained high medical relevance. These important human pathogens cause diverse diseases including trachoma and wide spread sexually transmitted diseases. *Chlamydia* establishes membrane bound inclusions in the host cell and loots the host for nutritional requirements. Infections are usually recognized by the host immune system and eliminated systematically, by triggering apoptosis. However, the pathogen *Chlamydia* has evolved various strategies to prevent the detection as well as protect the invaded cell against apoptosis or any other form of cell death. The evolutionary conservation of cell death regulation has not been investigated in the order *Chlamydiales*, which also includes *Chlamydia*-like organisms with a broader host spectrum. The present study was aimed at investigating the apoptotic response of human cells infected with the *Chlamydia*-like organism *Simkania negevensis* (Sn).

Simkania infected cells exhibited strong resistance to apoptosis induced by intrinsic stress or by the activation of cell death receptors. Apoptotic signaling was blocked upstream of mitochondria since Bax translocation, Bax and Bak oligomerisation and cytochrome c release were absent in these cells. Caspases were differentially regulated upon Sn infection. Caspase-3 and -9 were not activated upon Sn infection and apoptosis induction; whereas caspases-8 was activated in Sn infected cells even without apoptosis induction. This indicates that, Sn utilizes death receptor association independent caspase activation for thriving in the host environment. Infected cells turned on pro-survival pathways like cellular Inhibitor of Apoptosis Proteins (IAP-1/2 and XIAP) and the Akt/PI3K pathway. Sn infection also

activated the pro-survival transcription factor NF- κ B. Blocking any of these survival pathways sensitized the infected host cell towards apoptosis induction, demonstrating their role in infection-induced apoptosis resistance. The NF- κ B mutant cells also showed reduced infectivity of Sn, which indicated an essential role of NF- κ B in Sn infection.

It was interesting to observe that, *Acanthamoeba castellanii*, a natural host of Sn, survived maintaining its trophozoite forms after infection with Sn upon starvation. The metacaspases, responsible for encystment could be regulated by Sn upon infection. This suggests an early level of gene regulation indicating how the pathogen evolved its ability to inhibit apoptosis in higher organisms.

The resistance to apoptosis pathways subverted in Sn-infected cells was similar but not identical to those modulated by *Chlamydia*. Together, the data supports the hypothesis of evolutionary conserved signaling pathways to apoptosis resistance as common denominators in the order *Chlamydiales*.

V. Zusammenfassung

Vertreter der Ordnung *Chlamydiales* sind obligat intrazelluläre gram-negative Bakterien mit einer zunehmenden medizinischen Relevanz. Diese Humanpathogene lösen verschiedene Krankheiten aus, unter anderem Blindheit und sexuell übertragbare Krankheiten. *Chlamydia* führt zur Ausbildung einer Membrans umschlossenen Inklusion innerhalb der Wirtszelle und entzieht dem Wirt die nötigen Nährstoffe. Infektionen können vom Immunsystem des Wirts erkannt und systematisch mittels Apoptose bekämpft werden. *Chlamydia* hat jedoch verschiedene Strategien entwickelt um der Erkennung durch das Immunsystem zu entgehen und um ihre Wirtszelle vor dem Zelltod zu schützen. Ob die Fähigkeit den Zelltod der Wirtszelle zu regulieren evolutionär innerhalb der Ordnung der *Chlamydiales*, welche auch Chlamydia-ähnliche Organismen mit einem breiteren Wirtsspektrum beinhalten, konserviert ist wurde bislang noch nicht untersucht. In dieser Arbeit wurde das apoptotische Verhalten humaner mit dem Chlamydia-ähnlichen Organismus *Simkania negevensis* (Sn) infizierter Zellen untersucht.

Mit Simkanien infizierte Zellen zeigen eine starke Apoptose-Resistenz, unabhängig ob diese über intrinsischen Stress oder durch die Aktivierung von Todesrezeptoren ausgelöst wurde. Die Apoptose-Signalkaskade wurde vor den Mitochondrien blockiert, da es weder zu einer Bax Translokation, Bax und Bak Oligomerisierung noch zur Cytochrom c Freisetzung in den infizierten Zellen kam. Auch Caspasen zeigten eine veränderte Regulation. Die Caspase-3 und -9 wurden während einer Sn-Infektion und Apoptose-Induktion nicht aktiviert. Die Caspase 8 jedoch ist während der Sn-Infektion unabhängig von einer Apoptose-Induktion aktiv. Diese Tatsache lässt vermuten, dass Sn sich eines von den Todesrezeptoren

unabhängigen Mechanismus der Caspaseaktivierung bedienen um in der Wirtszelle zu verbleiben. Infizierte Zellen zeigen eine Aktivierung verschiedener antiapoptotischer Signalwege wie der der Inhibitor of Apoptosis Proteins (IAP1/2 and XIAP)- und den Akt/PI3K Signalweg. Durch eine Sn-Infektion kommt es außerdem zur Aktivierung des Transkriptionsfaktors NF- κ B. Wird einer dieser Überlebenssignalwege blockiert zeigen die infizierten Wirtszellen eine erhöhte Sensitivität gegenüber einer Apoptoseinduktion, was wiederum die zentrale Rolle der infektionsvermittelten Apoptoseresistenz aufzeigt. Eine Zelllinie mit mutiertem NF- κ B zeigte eine verminderte Infektiosität von Sn, was die zentrale Rolle von NF- κ B in der Sn-Infektion unterstreicht.

Infektionsversuche mit Sn und dessen natürlichem Wirt *Acanthamoeba castellanii* zeigten, dass diese im Sn-infizierten Stadium die Aufrechterhaltung ihrer Trophozyten-Form nach Nährstoffmangel überlebten. Die Metacaspasen, welche für die Einkapselung verantwortlich sind konnten durch eine Sn-Infektion reguliert werden. Dies weist auf ein frühes Stadium der Genregulation hin und lässt vermuten wie die Pathogene die Fähigkeit zur Apoptose-Inhibition höherer Organismen erlangt haben könnten.

Die durch eine Sn-Infektion vermittelte Resistenz der Wirtszelle gegenüber Apoptose-Signalwegen ist ähnlich, jedoch nicht identisch zu der durch *Chlamydia* vermittelten Resistenz. Diese Ergebnisse unterstützen die Hypothese eines evolutionär konservierten Signalwegs der Apoptoseresistenz als allgemeiner Nenner in der Ordnung der *Chlamydiales*.

Introduction

1.1. *Chlamydiales*

The bacterial order *Chlamydiales* includes obligate intracellular bacteria that have a *Chlamydia*-like developmental cycle and at least 80% 16S rRNA or 23S rRNA gene sequence identity. They infect cells of vertebrates (causing relevant diseases) and amoebae, while similar particles have been reported in invertebrate species including coelenterates, arthropods and mollusks.

1.1.1. History

Chlamydia-like disease 'trachoma' has been described in ancient Chinese and Egyptian manuscripts. In 1907, Halberstaedter and von Prowazek took conjunctival scraping from infected individuals and inoculated into the eyes of orang-utans (Fields and Barnes 1999). They named the new organism they found Chlamydozoa. Similar inclusions were subsequently described in the conjunctival cells of babies with non-gonococcal ophthalmia neonatorum in the uterine cervix from their mothers and in the urethral epithelium from male patients with non-gonococcal urethritis. These particles were capable of passing filters that retained most other bacteria. This property, coupled with the inability of these agents to grow on artificial media, led to the erroneous belief that these agents were viruses. Later in 1932 similar particles were reported in birds with acute pneumonia, psittacosis (Rivers & Schwentker, 1932). The finding of a common complement-fixing antigen strengthened the idea that these agents are those of Lymphogranuloma venereum (LGV) and hence was first propagated in monkey brain. The term 'Chlamydia' (Gr. Chlamus, a cloak) appeared in the literature in 1945. In 1965 with the advent of tissue culture

techniques and electron microscopy, evidence for bacterial rRNA, ribosomes and cell wall structures in *Chlamydiae*, it became evident that they were not viruses (Graham, 1965). Thus these particles were set out for further studies and classification under the order *Chlamydiales*.

1.1.2. Taxonomy

For years, *Chlamydiales* was the only bacterial order that had just one family and one genus (the *Chlamydiaceae* and *Chlamydia*, respectively). In the 1990s, based on the divergence in the glycogen accumulation inside the inclusion (Gordon & Quan, 1965) and resistance towards sulfadiazine (Lin & Moulder, 1966) the family *Chlamydiaceae* contained two species, *Chlamydia pneumoniae* and *Chlamydia pecorum* [both now placed into the genus *Chlamydophila*]. New molecular diagnostic methods based on nucleic acid amplification led to *Chlamydiae* being discovered in tissues and cells never before reported (joints, atherosclerotic plaques, brains, amoebae) (Table 1.1) and associated with diseases of previously unknown etiology like reactive arthritis, Alzheimer's disease, coronary artery disease, etc led to the deposition of 40 more chlamydial strains in the American Type Culture Collection (ATCC). DNA-DNA re-association, in particular, was established as a tool for distinguishing species (70% homology) and genera (20% homology) (Amann et al, 1995; Schleifer & Stackebrandt, 1983; Wayne & Diaz, 1987). Based on 16S and 23S ribosomal RNA sequence analyses and taking into account recently identified obligate intracellular species with *Chlamydia*-like developmental cycles, including *Simkania negevensis* (Kahane et al, 1995) and the amoebae isolate *Parachlamydia acanthamoebae* (Amann et al, 1997). With all this existing findings, Everett et al

(1999) made the new taxonomy of the order *Chlamydiales* which split the former family *Chlamydiaceae* into two genera, *Chlamydia* and *Chlamydophila* [the name *Chlamydophila*, given by Hans Truper and Johannes Storz, means 'chlamydia-like'], encompassing nine species, and added three new known *Chlamydiaceae* families, the *Parachlamydiaceae*, *Waddliaceae* and *Simkaniaceae*. Later (Schachter et al, 2001) mentioned that as there is no sufficient sequence difference in the order *Chlamydiales*, a division of genus into *Chlamydophila* and *Chlamydia* is unnecessary. Hence a modified version of the phylogenetic tree of *Chlamydiales* is shown in Figure 1.1.

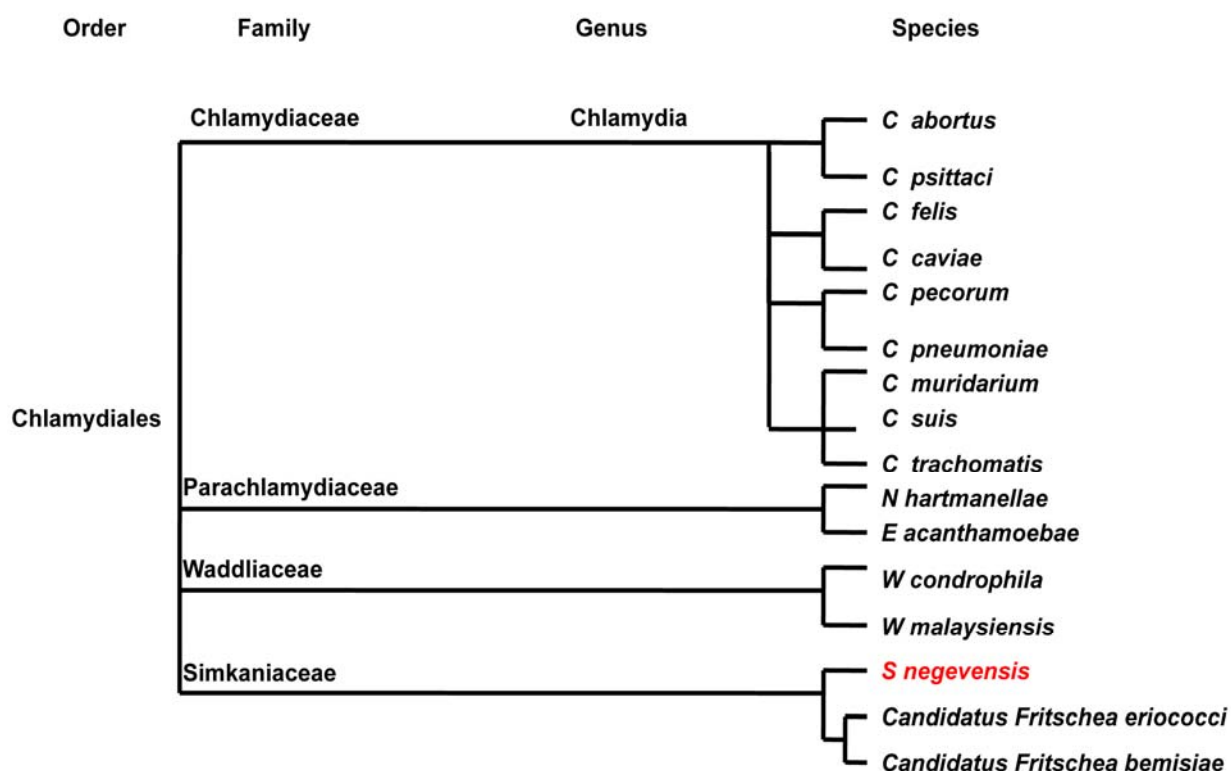


Figure 1.1: The phylogenetic tree of *Chlamydiales*. Based on the 16S and 23S ribosomal RNA sequence analysis, four families of *Chlamydiales* were classified with single genera in the family *Chlamydiaceae*. Subsequently 16 species (many serovars not mentioned) identified are classified above

with the respective hosts. The length of the lines does not represent the phylogenetic distance (modified from (Everett et al, 1999)). The pathogen under study is depicted in red.

Species	Host	Route of entry
<i>C.muridarum</i>	Mouse, hamster	Pharyngeal, genital
<i>C.suis</i>	Swine	Pharyngeal
<i>C. trachomatis</i>	Human	Pharyngeal, ocular, genital, rectal
<i>C. abortus</i>	Mammals	Oral, genital
<i>C. caviae</i>	Guinea pig	Pharyngeal, ocular, genital, urethral
<i>C. felis</i>	Cat	Pharyngeal, ocular, genital
<i>C. pecorum</i>	Mammals	Oral
<i>C. pneumoniae</i>	Human, frog, koala, horse	Pharyngeal, ocular
<i>C. psittaci</i>	Birds	Pharyngeal, ocular, genital
<i>S.negevensis</i>	Amoeba, human	Pharyngeal

(Modified after (Everett, 2000))

Table 1.1. List of different species in the genus *Chlamydia*, the specific hosts and the route of entry and site of infection.

1.1.3. Pathogenicity and epidemiology of *Simkania negevensis* (Sn)

Chlamydiae are obligate intracellular bacteria that cause a variety of acute and chronic diseases with high prevalence rate. The increase in reported chlamydial infections during the last 20 years reflects the expansion of clinical studies to understand better the virulence mechanism and the biology of the pathogen.

Discovered recently, *Simkania negevensis* is another obligate intracellular bacterium, isolated as a cell culture contaminant of unknown origin (Kahane et al, 1993). To date only one strain of *Simkania*, Z^T (ATCC VR-1471^T) (Everett et al, 1999) has been recognized. It has been suggested that Sn is an ubiquitous microorganism present in most aquatic habitats because of its relative resistance to commonly used procedures for routine treatment of drinking water supplies and its ability to replicate and exist in amoeba (Kahane et al, 1998). Later *Simkania* was reported as an emerging pathogen associated with several types of respiratory tract infection such as bronchiolitis in infants (Lieberman, Kahane et al. 1997; Kahane, Greenberg et al. 1998; (Greenberg et al, 2003; Greub, 2009), community acquired pneumonia (Guttmacher et al, 1997; Heiskanen-Kosma et al, 2008; Nascimento-Carvalho et al, 2009), chronic obstructive pulmonary disease in adults (Lieberman et al, 2002) and acute rejection in lung transplant recipients (Husain et al, 2007). Sn has also been amplified from an aortic aneurysm (Friedman et al, 2003). Moreover, seroprevalence rates in adults between 46–80% suggest a broad distribution of the organism in human populations (Lieberman et al, 1997). Sn has been suggested to represent a newly emerging pathogen because of its versatile infection capability (Friedman, Dvoskin et al. 2003; Kahane, Fruchter et al. 2007).

Simkania replicates in a biphasic life cycle similar to *Chlamydia*. Infection starts with an electron dense elementary body (0.2-0.3 μm), which differentiates into the electron lucent replicative form called the reticulate body (0.3-0.7 μm). The active replication cycle of Sn takes about 3–5 days and extensive long-term relationship with the host cell of about 10–15 days has been reported (Kahane et al, 2002). The strategy that this pathogen takes to keep its host alive for such a long period of time is unknown. Unlike other *Chlamydiales* (Kahane et al, 2002) observed that in Sn the replicative form may also be infective. This assumption was derived from the fact that they could observe similar kinetics of growth curve in less dense (RB) and more dense (EB) urografin fractions.

For decades research progress has been hampered to fully understand the genetics of *Chlamydiales* as they are obligate intracellular pathogens, there is no means to genetically manipulate them. Recently (Wang et al, 2011) had discovered that foreign DNA could be introduced into the chlamydial inclusion by using calcium ions. This will pave way for the chlamydial genetics and could lead to the development of chlamydial vaccines and therapeutic interventions.

1.1.4. The chlamydial life style

Chlamydiales have a unique biphasic life cycle. Bedson and colleagues first observed these distinct particles when they examined psittacosis-infected tissue (Bedson et al 1932). Later the existence of these developmental forms confirmed under electron microscopic studies (Constable, 1959; Gaylord, 1954). The pathogen exists in two morphological forms namely elementary body (EB), which is infective,

but metabolically inactive and reticulate body (RB), metabolically active and non-infective. The EB is 0.3 μm in diameter and RB around 1 μm . Infection is initiated by adherence of EB to the host cells through an unknown receptor that probably binds with heparan sulfate-like glycosaminoglycan present on the cell surface (Gutierrez-Martin et al, 1997; Kuo et al, 1973). Several other ligands for *Chlamydia* binding have also been proposed, including Hsp70 and Omp2 (Joseph & Bose, 1991; Raulston et al, 1998; Su et al, 1996; Swanson & Kuo, 1994; Ting et al, 1995). Recent studies further revealed the crucial role of the cellular PDGF- β receptor, the host kinase c-Abl, and the chlamydial protein Tarp (translocated actin recruiting phosphoprotein) in pathogen uptake (Clifton et al, 2004; Elwell et al, 2008). Together with other chlamydial effector proteins Tarp is translocated into the host cell via a type III secretion system (T3SS), a needle-like protein complex that spans the bacterial membranes (Subtil et al, 2000). Cytoskeleton rearrangements induce the uptake of the EB, which can also be seen in non-phagocytic cell (Jewett et al, 2008). After binding, the *Chlamydia* is internalized, enveloped within membrane-bound compartments that are subjected to bacteria induced modifications both in their luminal environment and in their membrane composition, and transported to a perinuclear location. These modified *Chlamydia*-containing membrane compartments are termed inclusions. The bacteria appear to survive within the inclusion in host epithelial cells through their ability to inhibit fusion between the inclusions and lysosomes (Eissenberg et al, 1983; Scidmore et al, 1996a; Scidmore et al, 1996b) whereas the fusion to sphingomyelinrich vesicles is enhanced (Hackstadt et al, 1995).

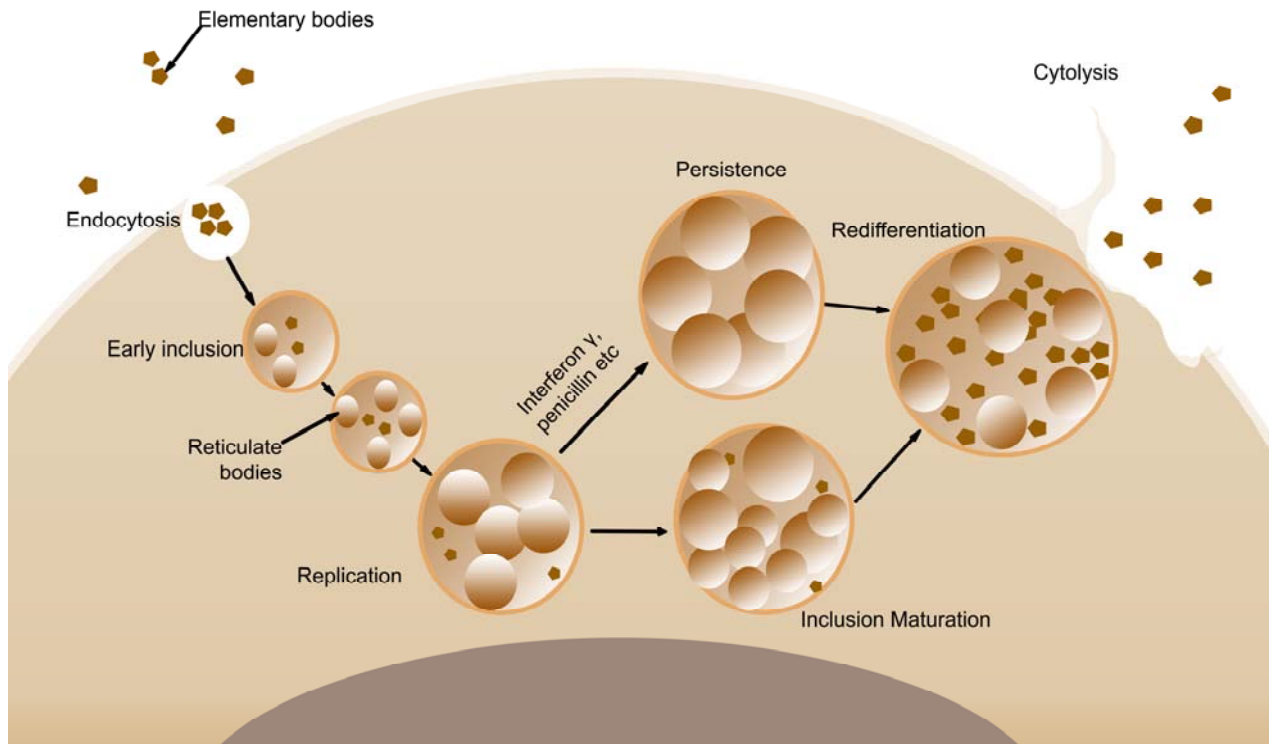


Figure 1.2. Infectious EB adhere to the receptors on the host cell. Upon internalization, the chlamydial inclusion is formed where EB differentiate into RB, which replicate by binary fission to produce several hundred particles that re-differentiate into infectious EB which leave the cell in order to start a new round of infection. Under certain conditions, such as sub-lethal doses of antibiotics like penicillin, IFN- γ stimulation or co-infection with virus, aberrant bodies can be formed to persist inside the host cell. Depending on the species, the developmental cycle is completed after 48-72 h or 5-8 days in tissue culture cell lines.

Within the inclusions, the EB differentiates into RB, which synthesize proteins and their own DNA and RNA then replicate by binary fission to form micro-colonies within the inclusion bodies. Differentiation of an EB into RB involves an increase in size, reduction of disulphide links in the outer membrane, unraveling of DNA in the condensed nucleoid and appearance of granular ribosomes (Wang et al, 1994). The initial signal for the differentiation of EB into RB is not known. By 18 hours post

infection (hpi), a proportion of the developed RB begins to transform back into EB while the remainder continues to divide in the growing inclusion (Hackstadt et al, 1999) within 24 h large inclusions are formed. Between 24 and 72 hpi the RB re-differentiate into EB and are released into the extracellular space by rupturing the cells to start a new round of infection (Moulder, 1991) as shown in Figure 1.2. As the RB is not infectious, re-differentiation into EB is an essential step in the chlamydial developmental cycle for the establishment of an acute infection. The engagement of the chlamydial type III secretion system in RB to EB re-differentiation was recently discussed by (Peters et al, 2007). The environmental signal that induces the reorganization from RB to EB is undefined. In the presence of Interferon γ , virus infection or antibiotics like penicillin the chlamydial particles gets stuck reversibly in the persistence stage where only aberrant bodies are observed. Persistence is the viable but non-cultivable growth stage of *Chlamydia* where it maintains long term relation with the host cells (Hogan et al, 2004). Depending on the species and the amount of bacteria that entered the cell, the developmental cycle of *C. trachomatis*, *C. pneumonia* and *Simkania negevensis* in cultured cell lines is completed after 48 h, 72 h and 5 days, respectively.

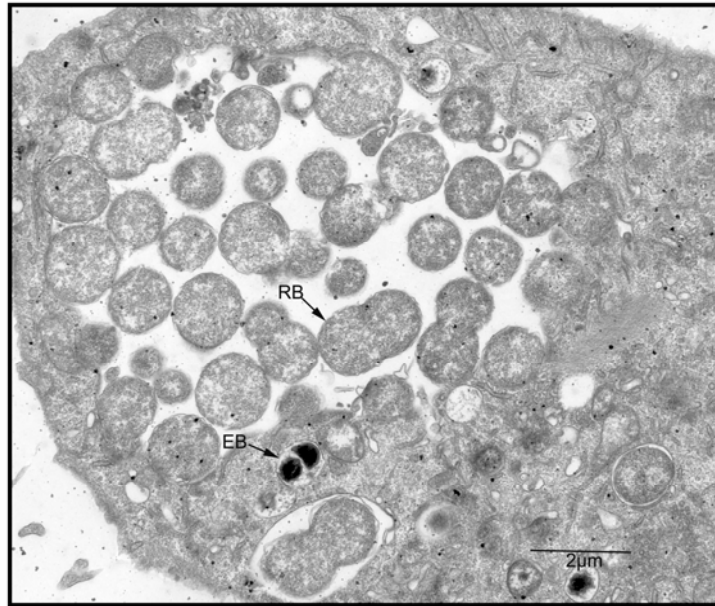


Figure 1.3. Transmission electron micrograph of intracellular *Chlamydia* in membranous vacuoles of an infected cervical cancer cell. Black arrowheads indicate the condensed elementary bodies (EB) and multiplying reticulate bodies (RB). Bar-2μm

1.2. Cell death: Evolution

Cell death has historically been subdivided into regulated and unregulated mechanisms. It is a fundamental cellular response that has a crucial role in shaping our body during development and in regulating tissue homeostasis by eliminating unwanted cells. The first form of regulated or programmed cell death (PCD) to be characterized was apoptosis, which was described in *Caenorhabditis elegans* in the early 1990s (Horvitz et al, 1994). PCD was first defined as the active physiological process of cell death depending on signaling events in the dying cell (Lockshin & Williams, 1965). Later different types of PCDs were characterized, including the apoptosis (type I PCD) and autophagy (type II PCD).

Apoptosis reflects a cell's decision to die in response to cues and is executed by intrinsic cellular machinery. Apoptosis involves controlled and well organized

events leading to cell death, in contrast the uncontrolled cell death (necrosis) entails a rapid loss of membrane integrity and release of cellular components into the extracellular space which leads to damage of neighboring cells and elicitation of immune response (Wyllie et al, 1980). A comparatively young type of PCD is pyroptosis. It can be described as a combination of apoptosis and necrosis as it both displays apoptotic characteristics and provokes inflammation (Cookson & Brennan, 2001). Due to its features resembling parts of necrosis, a fourth type of PCD has lately been proposed, termed pyronecrosis (Willingham, Bergstralh et al. 2007). Both the lack and excess of cell death are implicated in several relevant human diseases, including Alzheimer's disease (Loo et al, 1993) and Huntington disease (Portera-Cailliau et al, 1995), autoimmune disorders and cancer (Fukuhara et al, 1979; Tsujimoto et al, 1985)

Emerging evidence, however, suggests that the above said types of cell death do not adequately explain the various cell death mechanisms observed. Recent data point to the existence of multiple non-apoptotic, regulated cell death mechanisms, some of which overlap or are mutually exclusive with apoptosis (Degterev & Yuan, 2008). In addition to serving the maintenance of the body, the immune system activates PCD to eliminate the infected cell from the organism. Hence it is not surprising that the microbial pathogens have evolved a variety of strategies to modulate host cell death and subvert normal host defense response (Best, 2008).

1.2.1. Morphological and biochemical features of apoptosis

Apoptosis, the best characterized form of PCD, was coined by Kerr et al (1972) who termed this cellular phenomenon after the Greek saying “falling off leaves” (apo=off and ptosis=fall). Morphologically apoptosis is characterized by plasma membrane blebbing, cell body shrinkage (pyknosis), nuclear condensation and fragmentation (karyorrhexis), and formation of membrane bound cell fragments (apoptotic bodies). The apoptotic bodies consist of cytoplasm and tightly packed organelles enclosed within an intact plasma membrane that are rapidly phagocytosed *in vivo* by neighboring cells and resident phagocytes. This helps to prevent any inflammatory response, as the cytoplasmic content is not spilled into the extracellular milieu and the engulfment of apoptotic cells may actively prevent the production of inflammatory cytokines by macrophages and suppress dendritic cell maturation and antigen presentation (Brown et al, 2002). Biochemical features of apoptosis include a decrease in mitochondrial inner transmembrane potential, the activation of selective proteases leading to restrictive hydrolysis of more than 400 proteins, the cleavage of chromosomal DNA into internucleosomal fragments, the selective cleavage of various cellular proteins, and the translocation of phosphatidylserine from the inner to the outer leaflet of the plasma membrane (Salvesen and Riedl, 2008; Strasser et al., 2000). The main proteases involved in this extensive hydrolysis are members of caspase family (Chinnaiyan & Dixit, 1996) besides caspases, other proteases like lysosomal cathepsin, calpains and granzymes are also characterized in the apoptotic process (Lord et al, 2003). The specific morphological and biochemical features of apoptosis are manifestations of

evolutionarily conserved cell suicide machinery comprising of many apoptosis mediators described below.

1.2.2. Apoptosis-The fundamental mechanism of PCD

A simple pathway controls the primordial paradigm of PCD, described first in *Caenorhabditis elegans*. The initiation of apoptosis is regulated by transcriptional upregulation of Egl-1, a pro-apoptotic Bcl-2 homology-3 (BH3)-only member of the Bcl-2 protein family (Conradt & Xue, 2005). Binding of Egl-1 to anti-apoptotic CED-9 relieves the inhibition that CED-9 exerts on the adaptor protein CED-4, allowing CED-4 to bind and activate the cysteine protease CED-3, which in turn cleaves multiple specific cellular substrates to execute cell death (Metzstein et al, 1998) as described in Figure 1.4. Later, the mammalian homologues for the CED protein were revealed, though more complex, the mechanism seems to be highly conserved.

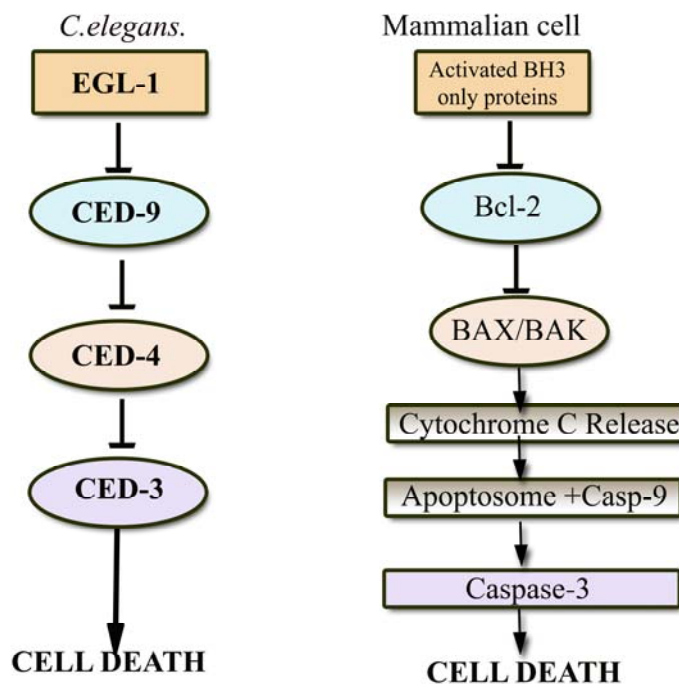


Figure 1.4. Comparison of cell death in *C. elegans* and mammalian cells. Extension of the apoptotic machinery can be observed at every step of the pathway, including BH3-only-protein activating signals, complex regulation of the Bcl-2 family and the addition of mitochondrial cytochrome c release, which drives the formation of an apoptosome and activation of the upstream caspases (first caspase-9 and then the executioner caspases, such as caspase-3 and caspase-7). Added complexity is provided by the existence of multiple family members in each class of the apoptotic regulators. These regulators provide 'fail-safe' apoptosis machinery that can generate specialized responses to various upstream stimuli.

1.2.3. Caspases-The Major class of apoptosis mediators

Caspases, the interleukin-1 β -converting enzyme (ICE) is a family of cysteine proteases (Chinnaiyan & Dixit, 1996). They are highly homologues to CED-3 in *C. elegans*. Fourteen different caspases are identified so far in humans (Alnemri et al, 1996), with three major functions, apoptosis activation, apoptosis execution and inflammatory mediation (Table 1.2). Caspases and their homologues are present in diverse species including nematodes, yeast and dipterans (Kumar & Dumanis, 2000).

The caspase family members share similarities in the amino acid sequence, structure and also the substrate specificity among each other (Nicholson & Thornberry, 1997). Caspases have an absolute requirement for cleavage after an aspartic acid in the substrate, but there is some exception to this rule that some caspases can cleave their substrate after a Glutamate (Hawkins et al, 2000). The protease activity of caspases is highly efficient, but not all proteins containing the tetrapeptide sequence X-Glu-X Asp are cleaved by caspases, implying that the

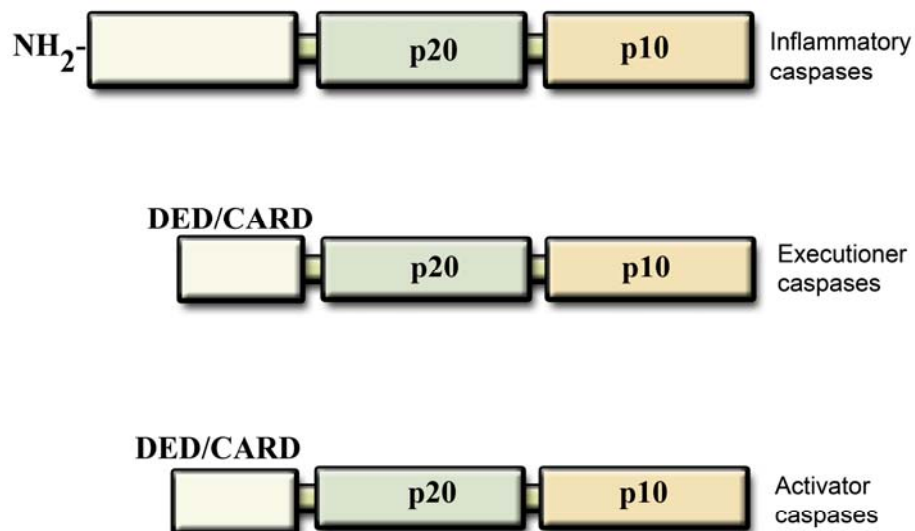
tertiary structural elements are also important for substrate recognition (Thornberry & Lazebnik, 1998). This strict substrate specificity explains why apoptosis does not entail indiscriminate protein digestion, but instead consists of cleavage of specific proteins in a coordinated fashion.

Caspases are synthesized as inactive zymogens in the cells and are activated either by autocatalytic processing by adaptor-protein mediated aggregation or by proteolysis by other active caspases (Thornberry & Lazebnik, 1998). Caspases are characterized by almost absolute specificity for aspartic acid in the P₁ position. Caspases contain three main domains: a pro-domain, large (p20) and small (p10) catalytic subunits (Thornberry & Lazebnik, 1998) as shown in Figure 1.5. The pro-domains of activator and inflammatory caspases contain protein–protein interaction domains (such as the caspase recruitment domain (CARD) and the death effector domain (DED) that link them to apoptosis signaling molecules (Degterev et al, 2003). The large domain contains the active site cysteine residue (Figure 1.5). All the caspases (ICE-like proteases) contain a conserved QACXG (where X is R, Q or G) pentapeptide active site motif. Activation of caspases involves the proteolytic cleavage of zymogens by auto-activation of pro-domain and activating other caspases to produce a heterodimer, two of which forms an enzymatically active heterotetramer (Figure 1.5). The activation of caspases can be initiated by the initiator caspases listed in Table 1.2, this in turn activate the downstream effector caspases. The autocatalytic cleavage of caspases is brought about by the close proximity by the adaptor proteins (Muzio et al, 1998). The CARD and DED domains interact with adaptor proteins to bring the caspases together for autocatalytic activity (Adams &

Cory, 2002). The caspase-8 gets activated by sequestering the adaptor protein Fas-Associated Death Domain (FADD) into the Death Inducing Signaling complex (DISC) (Muzio et al, 1998). Caspase-9 gets activated by forming a heteromeric complex, termed 'Apoptosome' with the adaptor protein Apoptotic Protease Activating Factor (Apaf-1) (Ahmad et al, 1998).

Subfamily	Role	Members
I	Apoptosis activator	Caspase-2,-8,-9,-10
II	Apoptosis executioner	Caspase-3,-6,-7
III	Inflammatory mediator	Caspase-1,-4,-5,-11,-12,-13,-14

Table 1.2. Subfamily of Caspases and their function. Based on the homology of the aminoacids the caspases are differentiated into three subfamilies with specific functions



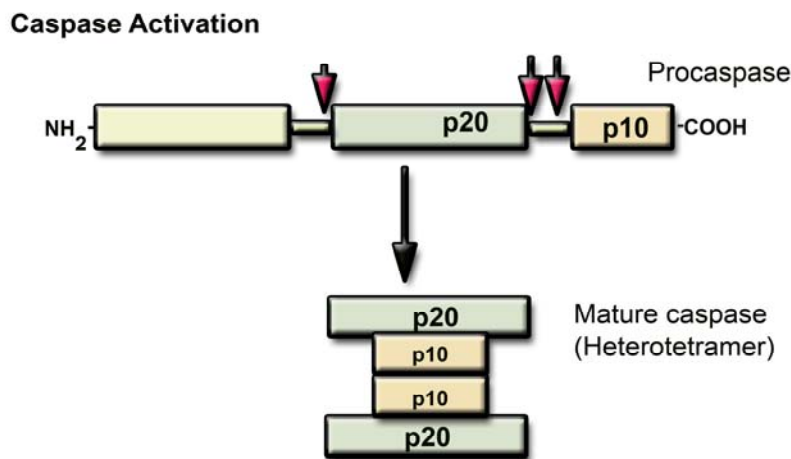


Figure 1.5. The sketch of the three major groups of caspases. The executioner and activator caspases have the DED/CARD domain, while the three different classes of caspases have the p20 and p10 domains. Scheme of pro-caspase activation. Cleavage of pro-caspase at the specific Asp-x- bonds leads to the formation of mature caspases, which comprises the heterotetramer (p20)₂-(p10)₂, and the release of the pro domains.

1.2.4. Consequences of caspase activation

During apoptosis, controlled demolition of the major structural components of the cell takes place. The activated executioner caspases, orchestrate the dismantling of the cell structures through cleavage of distinct critical cellular substrates, including poly (ADP-ribose) polymerase (PARP), lamins (Rao et al, 1996), fodrin (Martin et al, 1995), gelsolin, filamin (Kothakota et al, 1997) and DNA PK which are involved in DNA repair, hence this ensues the DNA degradation (Wyllie, 1980). In healthy cells, the caspase activated DNases (CAD) is found in complex with an inhibitor in the form of ICAD (Liu et al, 1997). During apoptosis the ICAD become the substrate of activated caspases and gets degraded liberating the CAD to enter the nucleus and

complete its activity of DNA fragmentation (Enari et al, 1998; Sakahira et al, 1998). Several components of the focal adhesion sites are targets of caspases like, focal adhesion kinases, tensin and components to cell-to-cell adhesions like catenins, cadherins are targets of caspases (Brancolini et al, 1997; Steinhusen et al, 2001). When all kinds of caspase substrates are activated, the cell will go through a series of changes, including the activation of related genes, a decrease in DNA damage repair ability, and the activation of zymogens or inactivation of enzymes, cytoskeleton disassembly, and chromatin fragmentation (Taylor, Cullen et al. 2008). The cell inevitably undergoes apoptosis.

1.2.5. Inhibitors of apoptosis (IAPs) the cellular inhibitor of caspases

The IAP proteins, which were originally identified in the genome of Baculovirus on the basis of their ability to suppress apoptosis in infected host cells (Miller, 1999), have also been found in mammals and fruit flies (Salvesen & Duckett, 2002a), but not in nematodes. There are eight mammalian IAPs, which include XIAP (X-linked IAP), c-IAP1, c-IAP2, ML-IAP (melanoma IAP)/Livin, ILP2 (IAP-like protein-2), NAIP (neuronal apoptosis-inhibitory protein), Bruce/Apollon and survivin. The hallmark of IAPs is the Baculoviral IAP repeat (BIR) domain, a ~80-amino-acid zinc-binding domain (Sun et al, 1999). The BIR domains fold as three-stranded β - sheet surrounded by four α helices that form a hydrophobic core with a Zn ion at the center. The RING domain of IAPs can confer E3 ubiquitin ligase activity to the IAPs conferring to self regulation of the IAP by the degradation by proteasome (Lorick et al, 1999). Other domains in IAPs include the caspase activation and recruitment domain

(CARD), phosphate loop and Ubiquitin Conjugating Domain (UBC) (Figure 1.6). The three BIR domains are responsible for mediating protein-protein interaction. Although similar they have specificities for distinct intermediates. BIR2 and BIR3 have been shown to directly bind and inhibit the proteolytic activity of caspases (Eckelman & Salvesen, 2006). BIR2 selectively targets caspase-3 and caspase-7 while BIR3 is specific for caspase-9 and can permanently remove caspases through the ubiquitylation mediated proteasome pathway (Shi, 2002). Interestingly caspase-9 binds to several IAPs but is selectively inhibited by XIAP, whereas caspase-3 and -7 are inhibited by XIAP, cIAP-1, cIAP-2 and NAIP (Salvesen & Duckett, 2002b). This difference occurs because of the difference in the mechanism of apoptosis inhibition. The cIAP-1 and -2 have a caspase-binding scaffold, while there is no caspase inhibitory activity (Eckelman & Salvesen, 2006). XIAP is hence the most potent among the IAPs, with its BIR2 domain specifically binding to the IAP binding motif of the active site of Caspases (Scott et al, 2005). As the RING domain has the E3 ubiquitin ligase activity, in addition to degrading caspase-3 and -7 they also undergo auto-ubiquitination and cross-ubiquitinate in a RING dependent manner during apoptosis (Yang et al, 2000).

The IAP mediated inhibition of caspases is antagonized by a family of proteins that contain IAP binding tetrapeptide motif, SMAC/DIABLO, released from the mitochondrial inter-membrane space. SMAC once released into the cytosol can promote the poly-ubiquitination of cIAP-1 and -2 leading to their degradation (Vaux & Silke, 2005a).

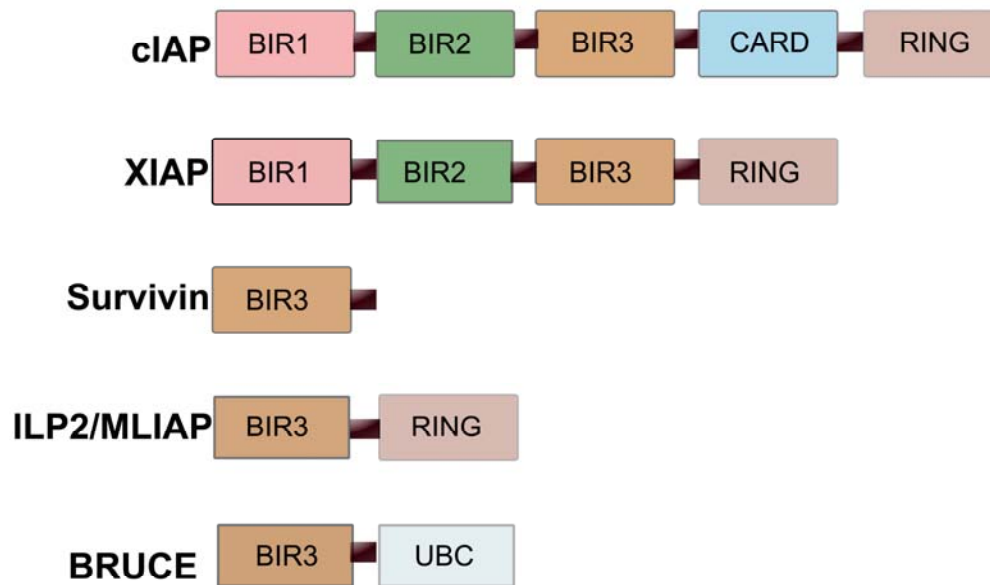


Figure 1.6. Molecular sketch of the cellular inhibitor of apoptosis protein. The cIAP-1/2 contains three baculoviral IAP repeat (BIR) domains with a CARD domain, while the CARD domain is absent in XIAP. A single BIR 3 domain makes the IAP, Survivin.

Survivin, which contains a single BIR domain, does not inhibit caspase activity in vitro (Ambrosini et al, 1997). Another single BIR containing IAP, ML-IAP/Livin, was reported to inhibit both caspase-3 and -9 although it does not seem to contain the sequence elements that are required for this inhibition.

1.2.6. The Bcl2 family

The first mammalian homolog for *ced-3* was described in 1988 as Bcl-2, which is involved in B-cell lymphomas (Vaux et al, 1988). Bcl-2 transfected B cells were shown to be resistant towards apoptosis normally induced in B cells by IL-3 withdrawal (Cleary et al, 1986; Tsujimoto et al, 1985): for the first time it was shown that the pathway toward tumorigenesis depends not only on the ability to escape

growth control but also depends on the ability to prevent apoptosis (Tsujimoto, 1989). The *bcl-2* gene codes for a 25 kDa protein. The C terminal 21 amino acids encode a stretch of hydrophobic amino acids that are important in membrane docking: Bcl-2 resides on the cytoplasmic face of the mitochondrial outer membrane, the nuclear envelope, and the endoplasmic reticulum. Deletion of the C terminus does not abrogate Bcl-2 survival function (Adams & Cory, 1998). Most Bcl-2 homolog has this hydrophobic C terminal domain, though they not necessarily are located on membranes but are cytosolic (e.g. Bax). While Bcl-2 and its most similar pro-survival homologs Bcl-x_L and Bcl-w contain all four BH domains, the other pro-survival members contain at least BH1 and BH2 (Cory & Adams, 2002) (Figure 1.7). Eighteen mammalian B-cell lymphoma protein-2 (Bcl-2) family members were identified and they are subdivided into three sub-classes: anti-apoptotic or pro-survival (Bcl-2, Bcl-x_L, Bcl-w, Mcl-1 and BFL-1/A1), multi-domain pro-apoptotic (Bax, Bok and Bak) and pro-apoptotic BH3-only (Bad, Bid, Puma, Noxa, Blik, BLK, HRK, BNIP3 and Bim, Bmf).

BH3-only proteins

The pro-apoptotic BH3-only proteins are the most apical regulators of this death-signaling cascade, and are activated by multiple stimuli from inside or outside the cell to initiate the apoptotic response. They are regulated transcriptionally, and by post-translational modifications such as phosphorylation, ubiquitination, and proteolytic cleavage. Their BH3 domain is an amphipathic α -helix that serves as a binding motif for interaction with a hydrophobic groove on either multi-domain anti- or pro-apoptotic Bcl-2 family members (Adams & Cory, 1998). This BH3 domain-mediated interaction of BH3-only proteins with multi-domain Bcl-2 family proteins

either antagonizes the survival activity of anti-apoptotic proteins or activates pro-apoptotic Bax and Bak, the antagonism of survival pathway is cooperated by the activation of Bax and Bak (van Delft et al, 2006). The Bax and Bak are kept in check in healthy cells by the specificity of BH3-only proteins.

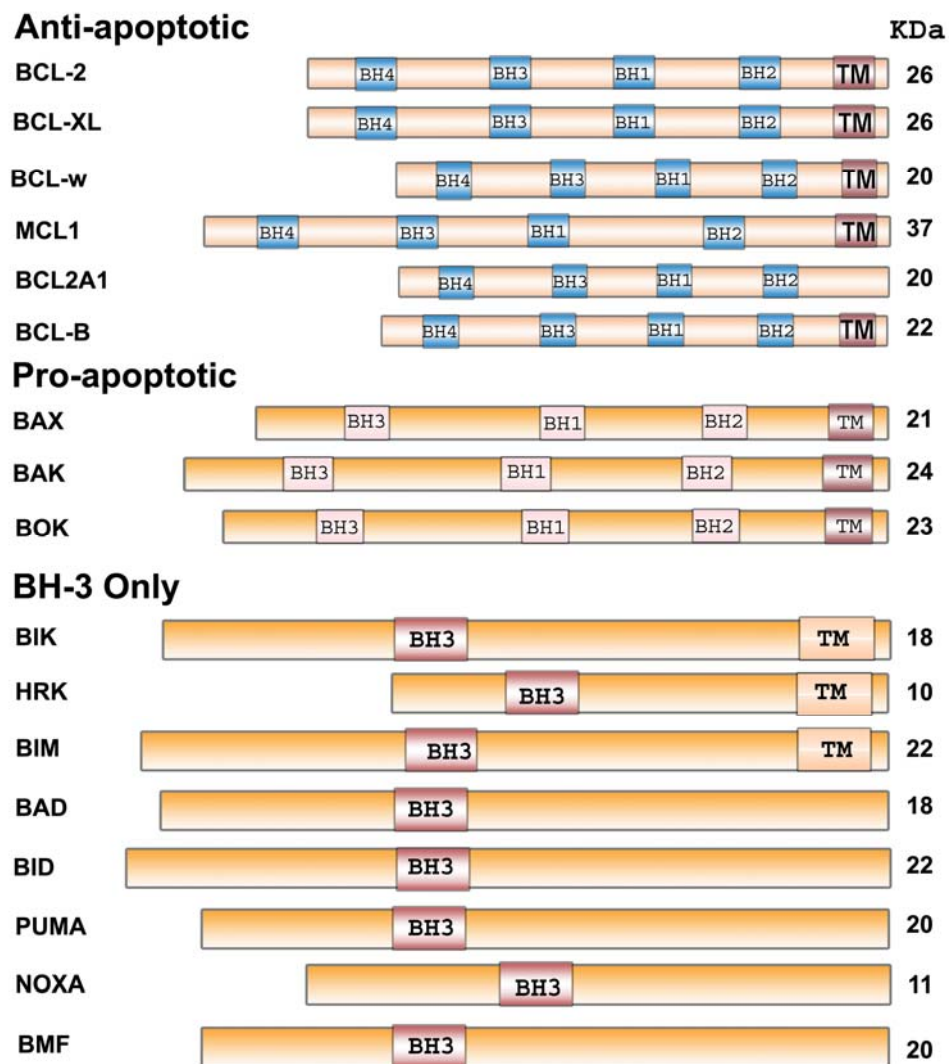


Figure 1.7. Pro- and anti-apoptotic family members can heterodimerize: the BH1, BH2 and BH3 domains of an anti-apoptotic member (e.g. Bcl-x_L) form a hydrophobic cleft to which a BH3 amphipathic alpha helix can bind (Sattler et al, 1997). This BH3 cleft coupling, reminiscent of ligand-receptor

engagement, may account for all dimerization within the family. Heterodimerization is not required for pro-survival function but is essential for the pro-apoptotic activity in the BH3 subfamily.

Bim is required for the removal of auto-reactive B and T cells thus play a role in autoimmunity (Bouillet et al, 2002). It is also induced by growth factor deprivation by class O forkhead box transcription factor-3A (FOXO3A) or by the transcription factors CEPB (CCAAT enhancer binding protein) or CHOP (CEBP homologues protein) in response to endoplasmic reticulum stress (Puthalakath et al, 2007). Bim and Bmf are associated with the microtubules and actin cytoskeleton respectively via interaction with Dynein light chains and their release can induce apoptosis (Puthalakath et al, 2001). It was recently reported that the BH3 peptides could induce mitochondrial fission and cell death in a Bax and Bak negative background (Shroff et al, 2009). Bim, a potent killer have high affinity to pro-survival proteins like Mcl-1 and Bcl-x_L thereby liberating Bax, which is now unconstrained the default state for cell death (Fletcher & Huang, 2006). Bim, tBid and Puma are known to activate Bax and Bak directly while Bad and Noxa lower the threshold of activation by neutralising pro-survival Bcl-2 (Cartron et al, 2004; Kuwana et al, 2002; Letai et al, 2002). It is also shown that tBid can induce cell death by release of cytochrome c in an Bax and Bak dependent way, and not in cells lacking one of these (Wei et al, 2001; Zong et al, 2001). This finding indicates that Bax and Bak lie downstream of BH3-only proteins.

Bax and Bak

The pro-apoptotic Bax remains in the cytoplasm in healthy cells, as its hydrophobic groove that serves as the receptor for the BH3-only proteins remain occluded by its C terminal trans-membrane domain. During death activation, activated

caspase-8 and tBid signal the conformational change of the protein, which leads to its oligomerisation and mitochondrial membrane localization, which leads to potential loss, and cell death (Annis et al, 2005; Antonsson et al, 2001). In contrast Bak is constitutively associated with the outer mitochondrial membrane where it forms large oligomeric complexes in response to apoptotic stimulus (Nechushtan et al, 2001). The Bak in healthy cells are sequestered by Mcl-1 and Bcl-x_L. While upon induction of apoptosis, Noxa dependent displacement of Bak from Mcl-1 followed by inactivation of Bcl-x_L takes place (Willis et al, 2005). Once Bax and Bak oligomers are formed, the mitochondrial permeabilisation is favored, resulting in the release of pro-apoptotic factors into the cytoplasm (Kroemer et al, 2007). Before cytochrome c release Bax and Bak induce the mitochondrial fragmentation (Martinou & Youle, 2006). The BH1 and BH2 domains of Bcl-2 family members (Bcl-2, Bcl-x_L and Bax) resemble membrane insertion domains of bacterial toxins: hypothetically they can form pores in organelles such as mitochondria, demonstrated in lipid bilayers in vitro. In yeast which lack Bcl-2 like proteins, CED-4 and caspases, Bax and Bak were shown to induce cell death, while Bcl-2 can protect, apparently by preventing mitochondrial disruption (Green & Reed, 1998). Bax and Bax-like proteins might mediate caspase-independent death via channel-forming activity, which would promote the mitochondrial membrane potential loss.

It is known that some of the BH3-only proteins like Bim and Puma, the 'direct activators of Bax and Bak are more potent apoptosis inducers than the 'derepressors' Bad and Noxa (van Delft & Huang, 2006). Studies show that Bim and Puma have high affinity to all pro-survival members, than other members (Chen et al, 2005b).

This suggests that Bcl-2 pro-survival proteins must be neutralized to induce apoptosis. This was confirmed when (Chen et al, 2005b) co-expressed proteins like Noxa (which neutralizes Mcl-1), and Bad (which neutralizes Bcl-2, Bcl_{xl} and Bcl-w) induced apoptosis in cells.

The anti-apoptotic Bcl-2 proteins

The Bcl-2 pro-survival proteins act by directly interacting with Bax and Bak. Bak form complexes with Mcl-1 and Bcl_{xl} by interacting with BH3 domain (Chen et al, 2005a; Letai et al, 2002). In contrast, the BH3 of Noxa is highly specific for Mcl-1 and BFL-1/A1. The BH3 of Bid and Bim are also capable of binding the grooves of multi-domain Bak and promoting their oligomerization, whereas other BH3 protein like Bad appeared more exclusive for binding to multi-domain of anti-apoptotic proteins such as Bcl-2 and Bcl_{xl} (Cheng et al, 2001). A central checkpoint of apoptosis is the activation of caspase-9 by mitochondria. The BH4 domain of Bcl-2 and Bcl_{xl} can bind to the C terminal part of Apaf-1 (Sattler et al, 1997), thus inhibiting the association of caspase-9 with Apaf-1 (Hu et al, 1998; Huang et al, 1998; Pan et al, 1998). This process seems to be conserved from nematodes to vertebrates since in *C. elegans* CED-9 binds to CED-4, preventing it from binding and activating CED-3. This collective type of data leads to the notion of discrete roles for BH3-only protein interactions governed by the binding specificity of their BH3 for multi-domain grooves. The Myeloid Cell Leukemia sequence-1 (Mcl-1) was identified as an early-induced gene during myeloblast cell differentiation. Mcl-1 is one of the most important anti-apoptotic proteins preventing inappropriate activation of Bax and Bak in healthy cells (Cuconati et al, 2003). Mcl-1 have C terminal trans-membrane domain that results in

its localization in the outer mitochondrial membrane (Yang et al, 1995), where it sequester Bak and maintain it in an inactive state. Recently, Sharma et al (2011) showed that the hypoxia-inducing factor (HIF-1 α) can stabilize the Mcl-1, which increases its anti-apoptotic effect.

1.2.7 NF- κ B, the master regulator

NF- κ B (Nuclear Factor-KappaB) was initially discovered and characterized as a transcription factor required for B- cell specific gene expression, later it was found to be ubiquitously expressed and required for the inducible expression of many genes (Sen & Baltimore, 1986). NF- κ B is a heterodimeric protein composed of different combinations of members of the Rel family of transcription factors, which are involved mainly in stress-induced, immune, and inflammatory responses (May & Ghosh, 1998). In addition, these molecules play important roles during the development of certain hemopoietic cells (Franzoso et al, 1997), keratinocytes, and lymphoid organ structures (Baeuerle & Henkel, 1994; Mattson & Camandola, 2001). More recently, NF- κ B family members have been implicated in neoplastic progression and the formation of neuronal synapses (Mattson and Camandola 2001). NF- κ B is also an important regulator in cell fate decisions, such as PCD and proliferation control, and is critical in tumorigenesis (Baldwin, 1996b). NF- κ B is composed of homo- and heterodimers of five members of the Rel family including NF- κ B 1(p50), NF- κ B 2 (p52), RelA (p65), RelB, and c-Rel (Rel) (Sen & Baltimore, 1986). Hetero and Homo-dimerization of NF- κ B proteins which exhibit differential binding specificities includes p50/RelA, p50/c-Rel, p52/c-Rel, p65/c-Rel, RelA/RelA, p50/p50, p52/p52, RelB/p50 and

RelB/p52 (May & Ghosh, 1998). All the Rel proteins contain a conserved N terminal region, called the RHD (Rel Homology Domain). The N terminal part of the RHD contains the DNA-binding domain, whereas the dimerization domain is located in the C-terminal region of the RHD. Close to the C terminal end of the RHD lays the NLS (Nuclear Localization Signal), which is essential for the transport of active NF- κ B complexes into the nucleus (Baldwin, 1996a). NF- κ B dimers are sequestered in the cytoplasm in un-stimulated cells via non-covalent interactions with a class of inhibitory proteins called I- κ B (Baeuerle & Baltimore, 1988b). There are seven I κ Bs, namely I κ B- α , I κ B- β , I κ B- γ (NEMO), I κ B- ϵ , Bcl-3, p100, p105. The I κ B have multiple copies of 30 repeating aminoacids called ankyrin repeats, which binds with NF- κ B and masks its NLS. Later (Baeuerle & Baltimore, 1988a) reported the inducible activation of NF- κ B in response to signals like Phorbol-12 myristate 13 acetate (PMA), which leads to the disruption of cytosolic I- κ B. The phosphorylation and degradation via ubiquitination of I κ B was later reported (Ghosh & Baltimore, 1990; Kerr et al, 1991) which releases the I κ B bound NF- κ B. I κ B degradation is a tightly regulated process and can be inhibited by proteasome inhibitors (Brown et al, 1995; Chen et al, 1995). The high molecular weight kinases, IKK (I κ B kinase), lead to the critical phosphorylation on Ser32 and Ser36 of I κ B that initiates its degradation (DiDonato et al, 1997; Mercurio et al, 1997). The Rel/NF- κ B proteins can be divided into two groups: Only RelA (p65), RelB and c-Rel contain potent TDs (Trans-activation Domains) within sequences C terminal to the RHD (Ganchi et al, 1992). In contrast, p50 and p52 do not possess TDs, and therefore cannot act as transcriptional activators by themselves (Ganchi et al, 1992).

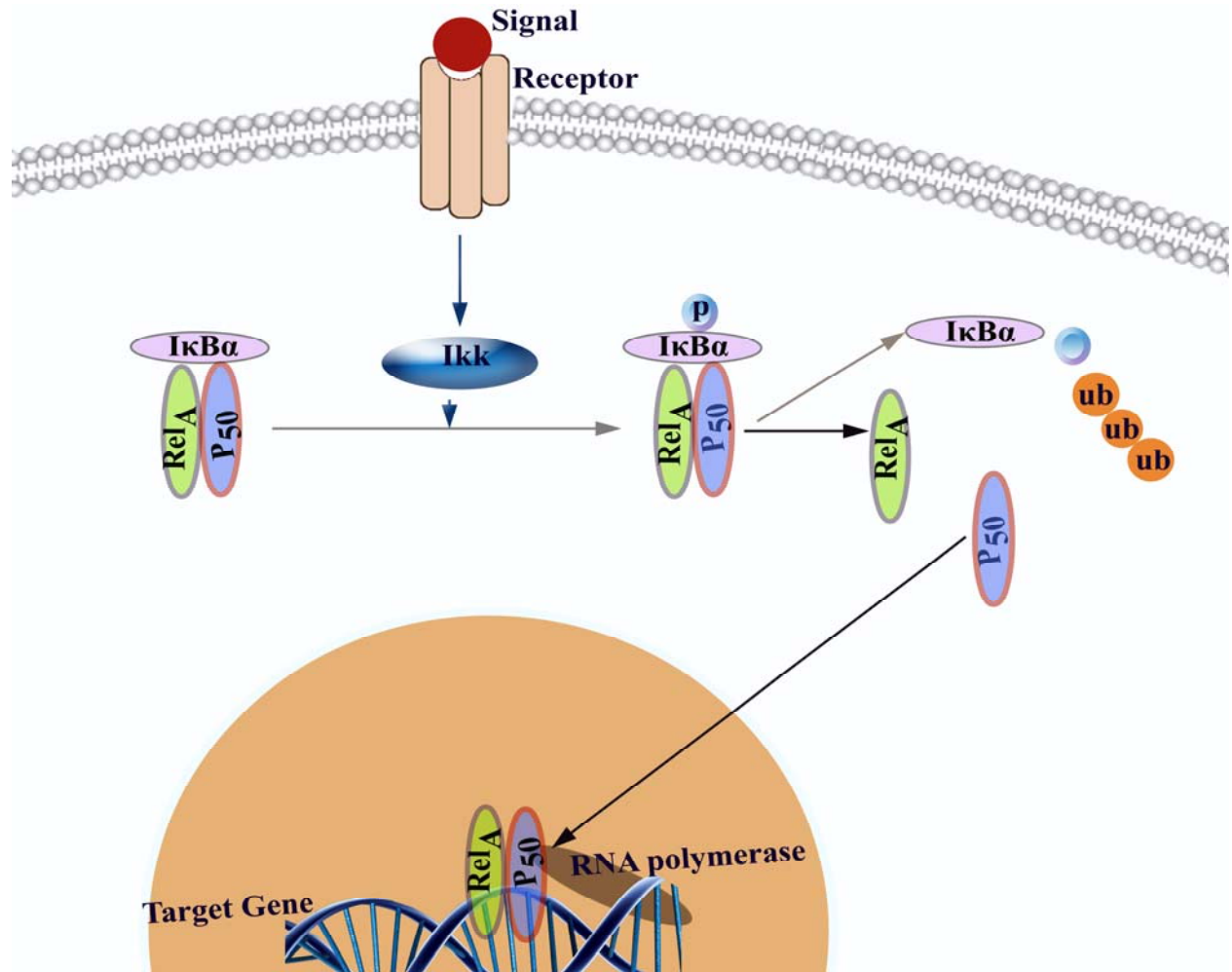


Figure 1.8. Mechanism of NF-κB activation. In an inactive stage the components of NF-κB is located in the cytosolic region complexed with the Inhibitor of kappa B (IκB). Upon activation with any extracellular signal, the Inhibitor of kappa B kinases (IKK) is activated and this in-turn phosphorylate the IκB, which results in its ubiquitination. The activated components of NF-κB then translocate to the nucleus and binds to specific DNA sequences called response elements. The DNA/NF-κB complex then recruits other proteins such as co-activators and RNA polymerase which results in downstream transcription of the target genes.

NF-κB-1 and NF-κB-2 are produced as p105 and p100 precursors, respectively (Fan & Maniatis, 1991). The NF-κB-1 p105 precursor appears to undergo constitutive processing by the cellular proteasome that removes the C terminal IκB-

like portion to generate p50. NF- κ B-2 p100 precursor can be processed to remove the I κ B-like C terminus, allowing the active p52 N terminal half to function in transcriptional regulation (Xiao et al, 2004a). Homo- or heterodimers of p50 and p52 were even reported to repress kappaB site-dependent transcription, possibly by competing with other transcriptionally active dimers (e.g. p50/RelA) for DNA binding (Heissmeyer et al, 2001).

NF- κ B can be activated by exposure of cells to LPS (Lipopolysaccharides) (Janssens et al, 2002) or inflammatory cytokines such as TNF (Tumour Necrosis Factor) or IL-1 (Interleukin-1), growth factors, lymphokines, oxidant-free radicals, inhaled particles, viral infection or expression of certain viral or bacterial gene products, UV irradiation, B or T-Cell activation, and by other physiological and non physiological stimuli (Dixit & Mak, 2002). The most potent NF- κ B activators are the proinflammatory cytokines IL-1 and TNF, which cause rapid phosphorylation of I κ Bs at two sites within their N terminal regulatory domain (Baldwin, 1996a). TNF, which is the best-studied activator, binds to its receptor and recruits a protein called TRADD (TNF-Associated Receptor Death Domain) (Ermolaeva et al, 2008; Wallach et al, 1999a). TRADD binds to the TRAF2 (TNF Receptor-Associated Factor-2) that recruits NIK (NF- κ B -Inducible Kinase) (Hsu et al, 1996; Sakurai et al, 2003). Both IKK1 and IKK2 have canonical sequences that can be phosphorylated by the MAP (Mitogen Activated Protein) kinase NIK/MEKK1 and both kinases can independently phosphorylate I κ B-alpha or I κ B-beta (Figure 1.8). TRAF2 also interacts with A20, a zinc finger protein whose expression is induced by agents that activate NF- κ B. A20 functions to block TRAF2-mediated NF- κ B activation (Song et al, 1996). A20 also

inhibits TNF and IL-1 induced activation of NF- κ B suggesting that it may act as a general inhibitor of NF- κ B activation (Lee et al, 2000).

1.2.8. The Akt/PKB signaling pathway

Akt also known as protein kinase B is a serine threonine protein kinase (Bellacosa et al, 1991) that plays a critical role in glucose metabolism, cell proliferation, apoptosis and cell migration (Datta et al, 1999). Akt possesses a protein domain called PH domain (plekstrine domain) which has high affinity to phosphoinositides (Franke et al, 1997). Akt is activated by upstream signaling events, as a consequence of the activated second messenger phospholipid kinase phosphatidylinositol 3-kinase (PI3K) (Brazil & Hemmings, 2001; Nicholson & Anderson, 2002). Activated receptor tyrosine kinases activate PI3 kinases directly or through tyrosine phosphorylation of scaffolding adaptors like IRIS. The binding of PI3-K generated phospholipids to the PH domain of Akt causes the translocation of Akt from cytoplasm to the plasma membrane (Downward, 1998). This brings Akt in close proximity to membrane bound protein kinase 3-phosphoinositide dependent protein kinase-1 and -2. PI3K phosphorylates PIP₂ (phosphatidylinositol 3, 4 bisphosphate) to PIP₃ (phosphatidylinositol 3, 4, 5 triphosphate) (Stokoe et al, 1997). These lipids serve as plasma membrane docking sites for proteins that harbor pleckstrin-homology (PH) domains, including Akt and its upstream activator PDK1 (Rong et al, 2001). Once bound to PIP₃, Akt can be phosphorylated by its kinases at threonine 308 and serine 473 (Alessi et al, 1997; Sarbassov et al, 2005). Activated Akt can go on to activate or deactivate myriad of substrates. One of the most important functions

signaling downstream directly or indirectly is to regulate the cell survival (Zhou et al, 2000). Akt enhances the survival of cells by blocking the function of pro-apoptotic proteins and processes. Akt negatively regulates the function or expression of several BH3-only proteins, which exert their pro-apoptotic effects by binding to and inactivating pro-survival Bcl-2 family members.

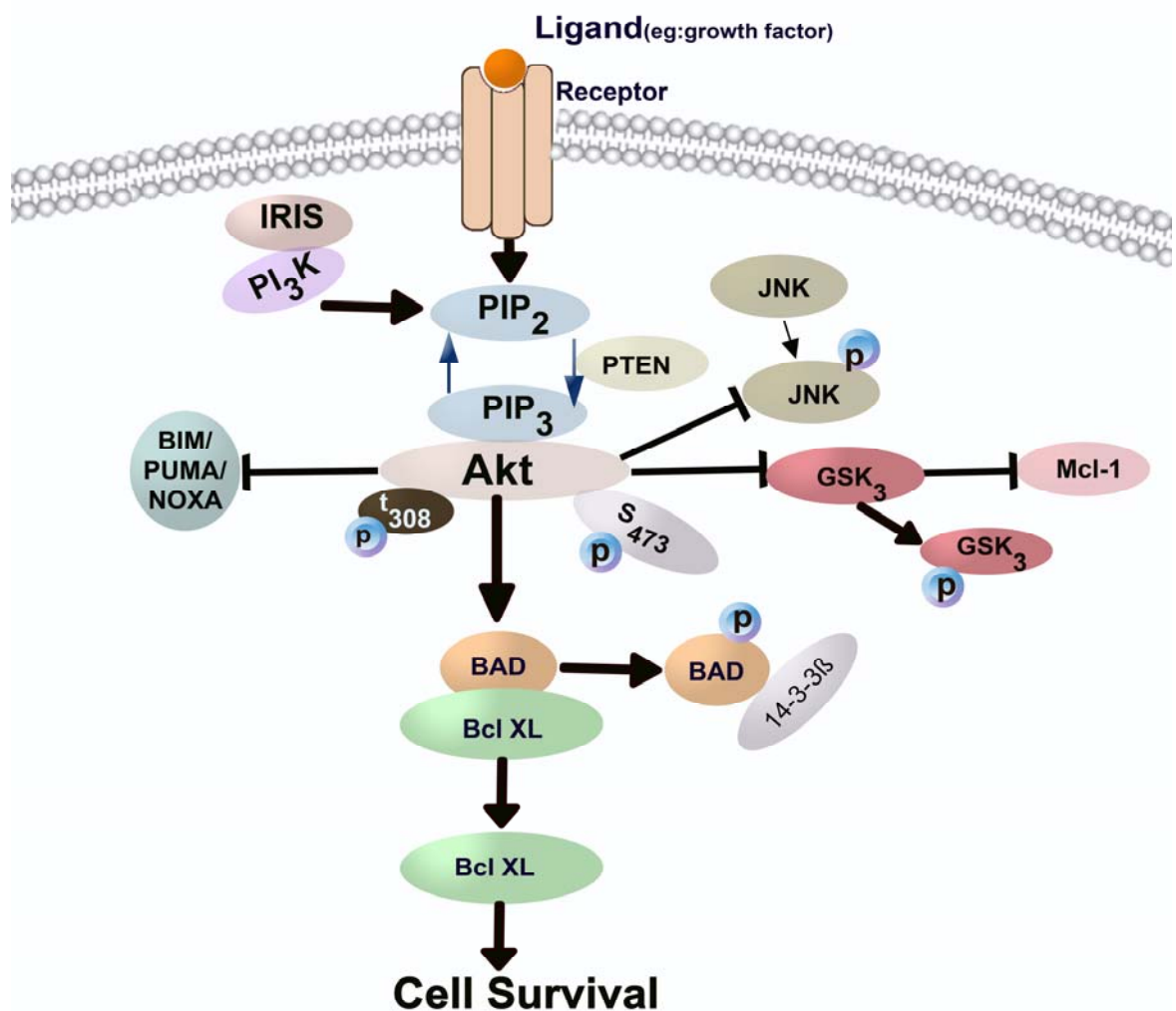


Figure 1.9. Overview of the Akt activation and consequences after the binding of diverse array of growth factors and cytokines to the receptor. Binding of p85 subunit of PI3K activates the conversion of PIP₂ to PIP₃, which recruits the Akt from the cytosol to the plasma membrane where its conformation

change and phosphorylation by PDK1 takes place. This phosphorylates a wide range of protein substrates (like Bcl2, BAD, MDM2, GSK3, IKK- β) thus regulating cell cycle and survival.

For instance, Akt directly phosphorylates and inhibits the BH3-only protein Bad (Datta et al, 1997; Zha et al, 1996). Survival factors stimulate Akt mediated phosphorylation of Bad on S136, and this creates a binding site for 14-3-3 proteins, which triggers release of Bad from its target proteins (Datta et al, 2000). The ability to phosphorylate S136 on Bad is important for the survival effects of Akt on neurons and other cell types (Zhou et al, 2000). Akt also inhibits the expression of BH3-only proteins like Bim through effects on transcription factors, such as FOXO and p53 (Zhu et al, 2008). Akt phosphorylates FOXO1 on T24, S256, and S319, and it phosphorylates FOXO3a and FOXO4 on three equivalent sites (Lee et al, 2011). Akt phosphorylation of FOXO proteins occurs in the nucleus, and, as with Bad, phosphorylated T24 and S256 are bound by 14-3-3 proteins, which displace FOXO transcription factors from target genes and trigger their export from the nucleus (Brownawell et al, 2001). Through this mechanism, Akt blocks FOXO-mediated transcription of target genes that promote apoptosis, cell-cycle arrest, and metabolic processes. Akt also targets the phosphorylation and deactivation of another transcription factor MDM2 that transcriptionally regulates P53 (Mayo & Donner, 2001; Ogawara et al, 2002). BH3-only proteins Puma and Noxa are important transcriptional targets of P53. Another important regulation is the phosphorylation of GSK3 (Fang et al, 2000), which inhibits the pro-survival Bcl-2 family member Mcl-1 (Flusberg et al, 2001). Under certain conditions Akt is also known to activate NF- κ B pro-survival pathway also it blocks apoptosis induced by p38/JNK activation (Faissner et al,

2006). The Akt pathway with respect to apoptosis inhibition and cell survival is depicted in Figure 1.9.

1.2.9. The extrinsic pathway of apoptosis

The extrinsic pathway begins outside the cell through the activation of specific pro-apoptotic receptors on the cell surface. These extracellular death receptor ligands such as tumor necrosis factor (TNF) (Locksley et al, 2001; Schulze-Osthoff et al, 1998), Fas ligand (FasL)/CD95L, and TNF-related apoptosis-inducing ligand (TRAIL)/Apo2L bind to their respective transmembrane receptors TNFR, Fas/CD95 and DR4/DR5 respectively (Peter & Krammer, 2003; Strasser et al, 2000). Fas, one of the best-characterized death receptors, play crucial roles in a variety of immunological processes. This is reflected in the fact that mutations in the gene encoding Fas underlie most cases of autoimmune lymphoproliferative syndrome (ALPS), an autoimmune disease in children characterized by massive lymphadenopathy, peripheral accumulation of doubly negative T cells, and autoantibody production leading to hepatosplenomegaly, hemolytic anemia, and thrombocytopenia (Straus et al, 1999). In an extensively characterized FasL/FasR and TNF- α /TNFR systems, clustering of the receptors occur together with the binding of the homologous trimeric ligand (Chan et al, 2000). Consequently, cytoplasmic adapter protein gets recruited to the receptor/ligand through the death domain. The binding of TNF- α to the TNFR, with a simultaneous block in protein synthesis, results in the binding of TRADD (TNFR associated death domain) with FADD (Fas associated death domain) and RIP (Hsu et al, 1995). Binding of TNF- α to the TNFR

can lead to activation of NF- κ B when protein synthesis is not blocked (Legler et al, 2003). Receptor aggregation in response to the pro-apoptotic Fas ligand binding and TNF initiates the formation of specific intracellular death-induced signaling complexes (DISCs) (Micheau & Tschopp, 2003; Peter & Krammer, 2003), where the adaptor molecule Fas-associated death domain (FADD) serves as platform for recruitment and bringing the pro-caspases to close proximity facilitating autocatalytic activity and activation of caspases-8 and -10 (Figure 1.10). The activation of caspase-8 in turn cleave downstream caspases, such as caspase-3 and caspase-7, to execute cell death; alternatively, caspase-8 can cleave the BH3-only pro-apoptotic protein Bid, which in turn amplifies the cell death signal by causing mitochondrial damage and cell death (Peter & Krammer, 2003). DISC formation is also modulated by several inhibitory mechanisms, including c-FLICE inhibitory protein (c-FLIP), which exerts its effects on the DISC by interacting with FADD to block initiator caspase activation; and decoy receptors, which can block ligand binding or directly abrogate pro-apoptotic receptor stimulation (Ashkenazi, 2008; French & Tschopp, 1999).

It has been shown that activation of the extrinsic pathway through the binding of CD95L/FasL to CD95/Fas can result in 2 apoptotic programs, termed type I and type II. Type I cells are able to overcome the need for mitochondrial amplification of the death signal in CD95-mediated apoptosis by producing sufficient amounts of caspase-8 at the DISC to directly cleave and activate effector caspases and execute cell death (Scaffidi et al, 1998). Because type I cells bypass mitochondrial involvement in CD95-mediated apoptosis, expression of Bcl-2 or Bcl-x_L has no inhibitory effect on their apoptotic program. Conversely, type II cells produce minimal

amounts of active caspase-8 at the DISC and require the mitochondrial amplification of the CD95 signal (Scaffidi et al, 1998). The signaling to mitochondria is probably through the pro-apoptotic BH3 domain of the Bcl-2 family member, Bid. The cleavage of Bid by caspase-8 (Li et al, 1998) results in its translocation to the mitochondria where it initiates the release of mitochondrial factors, which in turn augment cell death. Because type II cells rely on the apoptotic function of mitochondria, expression of Bcl-2/Bcl-x_l does confer protection from CD95-mediated apoptosis.

An explanation for the differences between type I and type II cells remains unclear, although differential expression of inhibitors of the death receptor signaling cascade, such as c-FLIP or XIAP, has been suggested to play a role (Walter et al, 2008).

1.2.10. The intrinsic pathway of apoptosis

As the name suggests the intrinsic pathway is triggered by severe cell stress like DNA damage, a defective cell cycle and detachment from the extracellular matrix, hypoxia and loss of cell survival factors. The intrinsic apoptotic pathway hinges on the balance of activity between pro- and anti-apoptotic members of the Bcl-2 super family of proteins, which act to regulate the permeability of the mitochondrial membrane (Coultas & Strasser, 2003). Members of the Bcl-2 family contain signature domains of homology called Bcl-2 homology (BH) domains as described above. Each of the BH3-only protein acts as sensor to the cellular stress (Bouillet & Strasser, 2002).

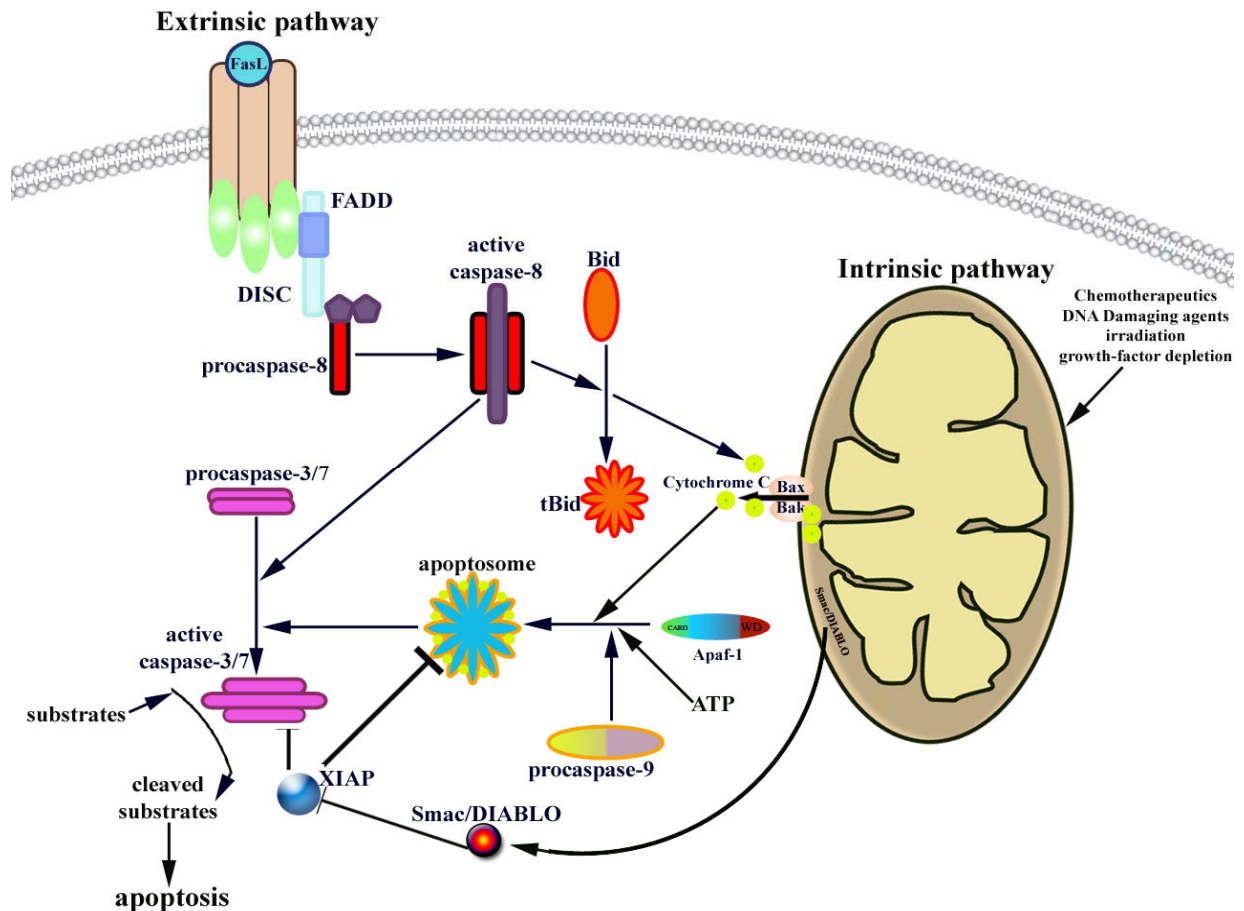


Figure 1.10. The intrinsic and extrinsic pathway of apoptosis. The extrinsic pathway is initiated by the death receptor ligation, which induces recruitment of FADD and pro-caspase-8 to death inducing signaling complex. Auto activation of caspase-8 can directly activate caspase-3 in type I cells. In type II cells amplification of the death signal via mitochondria is required which is mediated by Bid. Bax and Bak activation leads to mitochondrial membrane potential loss and apoptogenic factors are released into the cytosol. In the intrinsic pathway death inducing stimuli like DNA damaging agents leads to activation of BH3-only proteins accompanied by the down regulation of Bcl-2 like proteins.

BH3-only proteins activate the multi-BH domain pro-apoptotic proteins Bax and/or Bak, which then allow for permeabilization of the mitochondrial membrane. The anti-apoptotic Bcl-2 proteins Bcl-2 and Bcl-x_L act to prevent permeabilization of the outer mitochondrial membrane by inhibiting the action of the pro-apoptotic Bcl-2

proteins Bax and/or Bak (Figure 1.10). Upon membrane permeabilization, cytochrome c and the pro-apoptotic protein SMAC/DIABLO are then able to translocate from the intermembrane space of the mitochondria into the cytosol. As part of the intrinsic apoptotic pathway, the SMAC/DIABLO protein released from the mitochondria promotes apoptosis by directly interacting with IAPs and disrupting their ability to inactivate the caspase enzymes (Srinivasula et al, 2000). Hence, the intrinsic pathway is sometimes referred to as the mitochondrial pathway. Upon release from the mitochondria, cytochrome c forms a complex in the cytoplasm with adenosine triphosphate (ATP), an energy molecule, and the adaptor Apaf-1, forming a large multiprotein structure known as the apoptosome. Assembly of the apoptosome is highly regulated and may be driven by nucleotide exchange factors and/or ATPase-activating proteins. The primary function of the apoptosome seems to be multimerization and allosteric regulation of the catalytic activity of caspase-9. Initiator caspase-9 is recruited into the apoptosome and activated from within the adaptor protein complex, which in turn activates the downstream effector caspases-3, -6, and/or -7 (Thornberry & Lazebnik, 1998). Besides the release of cytochrome c from the intra-membrane space, the intra-membrane content released also contains apoptosis inducing factor (AIF) to facilitate DNA fragmentation and chromatin condensation. It is involved in initiating caspase independent pathway of apoptosis.

1.2.11. Perforin/granzyme pathway

In the granzyme B pathway, Perforin and granzyme B are released by cytotoxic T lymphocytes when they recognize antigen bearing cells (Zhao et al, 2006). Granzyme B is exophytically released through the plasma membrane with the aid of

the trans-membrane pore forming protein perforin (Shi et al, 1997). Once inside the cell it can directly activate caspase-3 or specifically cleave Bid and initiate the intrinsic pathway of cell death (Goping et al, 2003). Granzyme B can cleave proteins at aspartate residues and thus activate pro-caspase-10 and can cleave factors like ICAD (Sakahira et al, 1998).

1.3. Manipulation of host cell death pathway during microbial infections

Other than maintaining the homeostasis of the immune system, host cell death is a major factor determining clinical progression and disease severity in host pathogen interactions. The clearance of infected host cells is necessary to inhibit microbial replication and dissemination. Several forms of host cell death have been described during infection, as part of the host defense system or as a component of the survival strategy of the pathogen. The type of death the cell undergoes depends on the nature of the pathogen, pathogen load and site of infection. It is thus not surprising that pathogens have evolved an array of toxins and virulence factors to modulate host cell death pathways. Apoptosis, necrosis, and pyroptosis constitute the three major cell death modes for elimination of infected cells. The cellular factors that comprise the cells death machinery and are prone to manipulation by pathogens are summarized in Figure 1.11, reviewed in (Bohme & Rudel, 2009; Lamkanfi & Dixit, 2010).

1.3.1. Regulation of apoptosis during infection

Cells induce intrinsic apoptosis pathway to restrict the growth and reproduction of many pathogens. Recently it was shown that induction of intrinsic

pathway limited the facultative intracellular pathogen *Legionella pneumophila* (Nogueira et al, 2009). Defective or delayed apoptosis can lead to amplified pathogenesis and tissue damage (Marriott et al, 2005). The extrinsic apoptosis pathway equally contributes to the resistance against pathogenesis, as deletion of FasL prevented apoptosis followed by *Pseudomonas aeruginosa* infection and this lead to hyper susceptibility to sepsis-associated lethality (Grassme et al, 2000; Jones et al, 2002). The induction of apoptosis is however not always protective to the host as the pathogens can hijack the apoptotic machinery to eliminate the immune response. Many pathogens like *Staphylococcus aureus* and *Listeria monocytogenes* produce toxins and other virulence factors that activate the host apoptotic machinery (Weinrauch & Zychlinsky, 1999), while other pathogens like *Yersinia enterocolitica* and *Salmonella typhimurium* interfere with the NF- κ B and MAP kinase signaling cascades and induces cell death (Collier-Hyams et al, 2002; Monack et al, 1996). A well known example of such significant disease pathogenesis and tissue damage is the rapid depletion of lymphocytes in patients infected with HIV (Badley et al, 2000). Obligate and facultative intracellular pathogens also benefit for preventing apoptosis to facilitate survival and replication. For instance the obligate intracellular pathogen like *Rickettsia rickettsii* stimulates NF- κ B signaling in infected vascular endothelial cells in order to prevent host cell death and to continue replicating unabated (Clifton et al, 1998). *Coxiella burnetii*, protects infected cells from apoptosis during the early invasive stages of infection, presumably by blocking cytochrome c release from mitochondria (Luhmann & Roy, 2007). Infection with *Neisseria gonorrhoeae* leads to the down-modulation of pro-apoptotic proteins Bim and Bad which accounts for

inhibition of host PCD. Another successful strategy to promote host cell survival is the phosphorylation of the extracellular signal regulated kinase Erk and Akt induced by a multitude of bacteria, including *Neisseria gonorrhoeae* (Howie et al, 2008), *Coxiella burnettii* (Voth and Heinzen 2009), and *Salmonella enterica* serovar *Typhimurium* (Knodler et al, 2005a). Thus, the induction or inhibition of host cell apoptosis is dependent on a delicate balance of pro- and anti-apoptotic strategies during host-pathogen interactions (Figure 1.11).

1.3.2. Regulation of necrosis during infection

Reports demonstrating the induction or inhibition of programmed necrosis are very limited. A vaccinia virus strain expressing the CrmA homolog B13R/Spi2 was recently demonstrated to induce necrosis in adipocytes and hepatocytes in wild-type mice, while necrosis was markedly attenuated in RIP3 knockout mouse (Cho et al, 2009). It was also reported that in murine cytomegalovirus infection RIP3 induced necrosis is suppressed by the viral inhibitor of RIP activation (Upton et al, 2010). The tools for characterizing and interfering with necrotic cell death are currently being developed like the recently generated RIP1-specific small molecule inhibitors (Degterev et al, 2008). Necrotic cell death was also shown in murine myoblast cells exposed to alpha toxin of the bacterial pathogen *Clostridium septicum*, the causative agent of clostridial myonecrosis (Kennedy et al., 2009). The reports investigating the *in vivo* consequences of inducing necrosis suggest that it may contribute to the capability of host to limit and clear the infection by removing intracellular replication

niches and by enhancing the host's defensive responses through the release of pro-inflammatory cytokines and endogenous danger signals.

1.3.3. Regulation of pyroptosis during infection

Shigella flexneri, the etiological agent of bacillary dysentery, was the first pathogen reported to induce pyroptosis in infected macrophages (Hilbi et al, 1998). Subsequent studies demonstrated pyroptotic death of macrophages and dendritic cells infected with *Salmonella typhimurium*, *Pseudomonas aeruginosa*, and *Legionella pneumophila* (Monack et al, 2001; van der Velden et al, 2003). All these pathogens induce caspase-1 activation through the Ipaf inflammasome. With the notable exception of *Shigella*, this happens following delivery of bacterial flagellin into the macrophage cytosol. Because *Shigella* lacks flagellin, it remains to be determined how this pathogen induces activation of the Ipaf inflammasome. As with necrosis, the destruction of intracellular replication niches and the release of inflammatory cytokines and endogenous alarmins such as HMGB1 may represent key mechanisms by which pyroptosis may contribute to the anti-infectious responses of the host.

1.3.4. Apoptosis and host cell modulation by *Chlamydiales*

Obligate intracellular bacteria, *Chlamydia* confer resistance to the host cell against a variety of apoptotic stimuli, including the action of cytotoxic T cells (Fan et al, 1998b). The bacteria are thus able to maintain a long-term relationship inside the host cell and complete their replication cycle inside the cell, at the end of which numerous elementary bodies are produced and released to infect other cells. *Chlamydia* can sometimes develop long-term chronic infections that could contribute

to diseases such as atherosclerosis. Protection of the host cell against apoptosis would acquire greater significance for the bacteria under such conditions. It is not surprising, therefore, that persistently infected cells have also been shown to be potentially resistant to various forms of apoptosis (Dean & Powers, 2001). Apoptosis resistance has been attributed to all major chlamydial species viz. *Chlamydophila pneumoniae*, *Chlamydia trachomatis*, *Chlamydophila psittaci*, *Chlamydophila caviae*, as well as *Chlamydia muridarum* (Coutinho-Silva et al, 2001; Fan et al, 1998b; Rajalingam et al, 2001a; Zhong et al, 2006). Of these, *C. trachomatis* and *C. pneumoniae* have been widely studied for their strong anti-apoptotic effect and relevance to human diseases, reviewed under Sharma and Rudel (2009). The chlamydial infection protects cells against different forms of apoptosis described above (extrinsic, intrinsic and granzyme B), mediated by various stimuli including staurosporine (STS), TNF- α , etoposide, granzyme B/perforin, and UV light (Fan et al, 1998b; Fischer et al, 2001; Rajalingam et al, 2001a) (Figure 1.11). *Chlamydia* has evolved several strategies to escape host immune response. *Chlamydia* can down regulate the expression of MHC class I and II molecules, thus avoid the recognition of host cells by CD⁺ T cells (Zhong et al, 1999; Zhong et al, 2000), they also release some soluble factors that prime the by-stander uninfected cells for less MHC class I expression which would promote more rapid immune evasion upon pathogen entry and help promote unfettered spread of infections (Ibana et al, 2011). Analysis of apoptosis pathway in *Chlamydia* infected cells showed that they resist the cytochrome c release from the mitochondria to the cytosol, caspase-9 activation and processing of caspase-3 was prevented as expected (Fan et al, 1998b). Later it was

also found that the infected cells fail to achieve activation of Bax and Bak, the regulators of mitochondria permeabilisation (Xiao et al, 2004b). *Chlamydia* infection leads to the *Chlamydia* protease like activity factor (CPAF) dependent broad scale degradation of BH3-only proteins (Dong et al, 2005; Paschen et al, 2008), but later Rajalingam et al (2008a) reported that there was no noticeable degradation of these pro-apoptotic proteins. It was recently reported that persistent chlamydial infection does not depend on CPAF for resistance to apoptosis (Rodel et al, 2012). *Chlamydia* infected cells resist host apoptotic machinery at different levels, not only at mitochondria level but also downstream of it (Fischer et al, 2001). *Chlamydia* also interferes with the host protein synthesis, upregulation and stabilization of certain anti-apoptotic proteins like cIAP-1, cIAP-2, XIAP and Mcl-1 (Paland et al, 2006b; Rajalingam et al, 2008a; Rajalingam et al, 2006a). Moreover, the significance of the anti-apoptotic proteins in conferring apoptosis resistance became clear from the RNAi technology reported in Rajalingam et al (2006a). RNAi screen to identify the critical host factors revealed Bcl-2 and Mcl-1 as the targets. Later it was observed that activation of Raf/MEK/ERK pathway is required for the stabilization of Mcl-1 (Rajalingam et al, 2008a). One another host factor that was activated and stabilized Mcl-1 was the transcription factor HIF-1 α (Sharma et al, 2011).

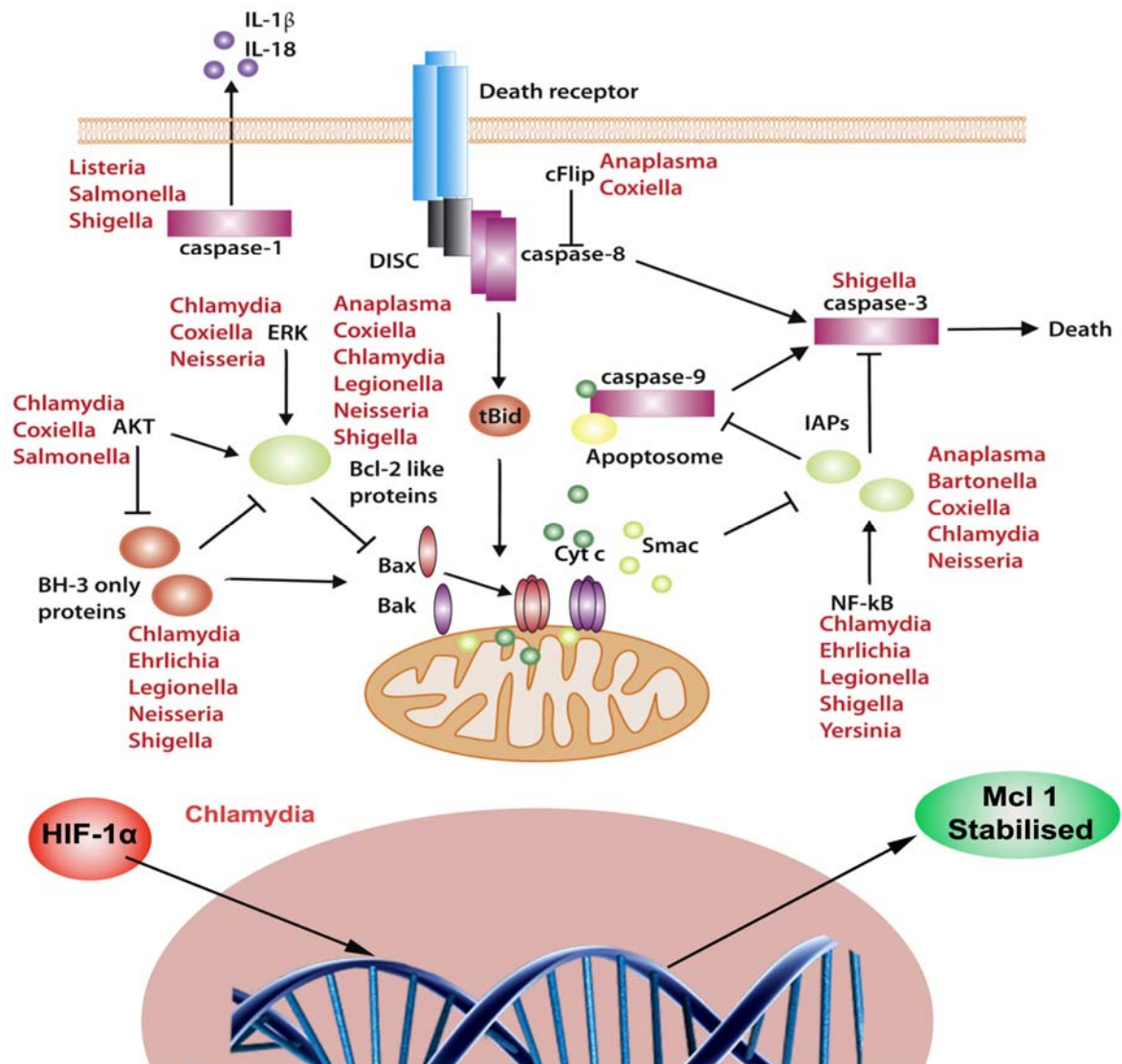


Figure 1.11. Modulation of cell death signaling cascades by bacterial pathogens. (Modified from (Bohme & Rudel, 2009)). Apoptosis is activated by intrinsic /extrinsic pathway. Bacterial pathogens (indicated in red) interfere at several points with either the regulators or executioners of the pathway.

1.4. Aim of the work

The present study aims at investigating the evolutionary conservation of infection induced cell death inhibition among *Chlamydiales*. The apoptotic response of human cells infected with the *Chlamydia*-like organism *Simkania negevensis* (Sn) was under study. Sn maintains a long-term relationship with the host cells, as they can infect and remain upto 14 days in cell cultures. This bacterium ensures to keep the cell healthy and alive until it completes its life cycle. This aroused the curiosity as how this pathogen regulates the host signaling and remains hidden from the host immune response. Hence, this study was aimed to find if and how Sn infection regulates the signaling pathways in host cells. The different cell death pathways upon induction with various cell death inducers in Sn-infected cells were aimed for investigation. It was interesting to explore how similar was the pathways subverted in Sn-infected cells compared to *Chlamydia*, as they belong to the same family. This work supports the hypothesis of evolutionary conserved signaling pathways to apoptosis resistance as common denominators in the order *Chlamydiales*.

2. Materials and methods

2.1. Materials

2.1.1. Cell lines used in the study

Cell lines	Features	Origin	Source/Donor
HeLa 229	Cervical adenocarcinoma	Human	ATCC CCL-2.1
HEp-2 cells	Laryngeal carcinoma	Human	ATCC CCL-23
HT1080 Wild type	Connective tissue (fibrosarcoma)	Human	ATCC CCL-121
HT1080 (I κ B mutant)	Connective tissue (fibrosarcoma) with I κ B under super repressor	Human	ATCC CCL-121

Table 2.1. Human tissue culture cell lines used in the study

2.1.2. Bacterial strain used in the study

Bacteria	Strain	Source/Donor
<i>Simkania negevensis</i>	Z	ATCC VR-1471 TM

Table 2.2. Bacterial strain used in the study

2.1.3. Amoebal strain used in the study

Amoeba	Strain	Source/Donor
<i>Acanthamoeba castellanii</i>	C3	ATCC 50739 TM

Table 2.3. Amoebal strain used in the study

2.1.4. Cell culture medium and buffers

Medium	Ingredients
Cell culture media (HeLa 229 cells)	1x RPMI 1640 + L-Glutamax + 25 mM HEPES (GIBCO, Germany), 10 % (v/v) heat inactivated FCS (Biochrom)
HT 1080 WT and IκB mutants	1x RPMI 1640+ L-Glutamax + 25 mM HEPES (GIBCO, Germany), 10 % (v/v) heat inactivated FCS (Biochrom)
<i>Simkania</i> culture media	1x RPMI 1640+ L-Glutamax + 25 mM HEPES (GIBCO, Germany), 10 % (v/v) heat inactivated FCS (Biochrom), Penicillin (100 U/ml), Streptomycin (100 µg/ml), Vancomycin (50µg/ml), Gentamycin (8 µg/ml), Cycloheximide (1 µg/ml)
Freezing media	1x RPMI 1640 + L-Glutamax + 25 mM HEPES (GIBCO, Germany), 10 % (v/v) heat inactivated FCS(Biochrom), 10 % (v/v) DMSO
Transfection media	Cell culture medium + 20% (v/v) Optimem (GIBCO)
SPG buffer	0.22 M sucrose, 10 mM Na ₂ HPO ₄ , 3.8 KH ₂ PO ₄ , 5 mM Glutamate
PEI stock solution	Dissolve PEI powder to a concentration of 2 mg/ml in water which has been heated to 80°C. Allow solution to cool to room temperature. Adjust pH to 7.0 with 5 M HCl. Filter sterilize. Freeze aliquots at -80°C.

Amoebal culture medium (Peptone yeast extract glucose (PYG))	Peptone (20g), glucose (18g), yeast extract (2g), sodium citrate (1g), $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ (980mg), $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ (355mg), KH_2PO_4 (340mg) per liter of medium. pH-6,7.
Encystment medium	95 mM NaCl, 5 mM KCl, 8 mM MgSO_4 , 0.4 mM CaCl_2 , 1 mM NaHCO_3 , 20 mM Tris-HCl, pH 9.0.

Table 2.3. List of medium and buffers used for cell cultures.

2.1.5. Buffer and Solutions

Buffers and solutions were prepared using Millipore Q-distilled water. Chemicals were purchased from Sigma (Deisenhofen, Germany) or Roth (Karlsruhe, Germany), unless indicated otherwise.

2.1.5. i. Buffer for Immuno fluorescence

Buffer	Ingredients
PBS (1x) (/L)	8 g NaCl, 0.2 g KCl, 2.68 g Na_2HPO_4 (1xH ₂ O), 0.24 g KH_2PO_4 , adjust to pH 7.4
Fixing buffer (/L)	1x PBS + 4% (w/v) PFA, adjust to pH 7.2
Permeabilization buffer	1x PBS + 0.2% (v/v) TritonX 100
Blocking buffer	1x PBS + 10% (v/v) FCS
Mowiol mounting medium	2.4 g Mowiol 488, 6 g glycerol, 6 ml H ₂ O, 12 ml 0.2 M Tris/HCl, adjust to pH 8.5

Table 2.4. Buffers and components used for immunofluorescence.

2.1.5.ii. Buffer for Immunoblotting

Buffer	Ingredients
10 x SDS buffer (/L)	30.275 g Tris, 144 g glycine, 10 g SDS
10x Semi dry buffer (/L)	24 g Tris, 113 g glycine, 2 g SDS
1x Semi dry transfer buffer	1x semi dry buffer + 20% (v/v) methanol
10x TBS (/L)	60.5 g Tris, 87.6 g NaCl, adjust to pH 7.5 with HCl
TBST ₂₀	1 x TBS + 0.5% (v/v) Tween ₂₀
Blocking solution	TBST ₂₀ + 5% (w/v) dry milk powder or BSA
Stripping buffer (500 ml)	7.5 g glycine, 0.5 g SDS, 1.54 g DTT, 5 ml Tween ₂₀ , Adjust to pH 2.2
2x Laemmli buffer	100 mM Tris/HCl [pH 6.8], 20% (v/v) glycerol, 4% (w/v) SDS, 1.5% (v/v) 2-mercaptoethanol, bromophenol blue
Lysis buffer for phospho protein	20 mM HEPES, 400 mM NaCl, 10 mM KCl, 20% (v/v) glycerol, 0.5% (v/v) Nonidet P-40, 1x Complete, 1x PhosSTOP
12% SDS lower gel solution	For 10 ml: 3.3 ml H ₂ O, 4 ml 30% (v/v) acrylamide:bisacrylamide mix (37.5:1), 0.1 ml 10% (w/v) SDS, 2.5 ml, 1.5 M Tris/HCl [pH 8.8], 0.1 ml 10% APS, 4 µl TEMED
SDS upper gel solution	For 5 ml: 3.4 ml H ₂ O, 0.83 ml 30% (v/v) acrylamide: bisacrylamide mix (37.5:1), 0.63 ml 1.0 M Tris/HCl [pH 6.8], 0.1 ml 10% (w/v) SDS, 0.05 ml 10% APS, 5 µl TEMED

Table 2.5. Buffers and components used for immunostaining.

2.1.6. Commercial Kits used in the study

Name	Purpose	Company/Donor
a. Caspases Glo-8 assay	Caspases-8 activation	Promega
b. DeadEnd™ Fluorometric TUNEL Kit	Measure apoptosis	Promega

Table 2.6. List of commercial kits used in the study.

2.1.7. Inhibitors, Inducers used in the study

Name	Purpose	Company / Donor
a. TNF- α	Apoptosis inducer	BD Pharmingen
b. LY 294002	PI3 kinase inhibitor	Cell Signaling
c. CAPE	NF- κ B inhibitor	Sigma
d. IKK-2 inhibitor IV	NF- κ B inhibitor	Calbiochem

Table 2.7. List of inducers and inhibitors used in the study.

2.1.8. Fine chemicals

Compound	Manufacturer
a. BMH	Sigma
b. Complete protease inhibitor	Roche
c. DRAQ5	Alexis
d. ECL immunoblotting substrate	Thermo
e. Hoechst 33342	Sigma
f. Syto 82	Invitrogen
g. Phalloidin	Invitrogen

h. Lipofectamine™ 2000	Invitrogen
i. PhoSTOP (phosphatase inhibitor)	Roche

Table 2.8. List of fine chemicals used in the study.

2.1.9. Antibodies

Name	Source	Company	Product #	Dilution	Application
Akt	rb	Abcam	93856	1:1000	IB
β-Actin	ms	Sigma	A5441	1:3000	IB
Bad	rb	Cell signaling	9292	1:1000	IB
Bax	rb	Abcam	16910-50	1:1000	IB/IF
Bak	rb	Santa Cruz	526	1:1000	IB
Bcl-2	ms	Santa Cruz	509	1:1000	IB
Bid	rb	Santa Cruz	11423	1:1000	IB
Bim	rb	Santa Cruz	2819	1:1000	IB
Bmf	rb	Cell signaling	4692	1:1000	IB
Caspase-3	rb	Cell Signaling	9665	1:1000	IB
Cl caspase-3	rb	Cell Signaling	9661	1:200	IF
Caspase-9	rb	Cell signaling	9502	1:1000	IB
clAP-1	rb	Abcam	2399	1:1000	IB
clAP-2	rb	Abcam	23423	1:1000	IB
Chla Hsp 60	ms	ThermoScientific	MA3-023	1:3000	IB/IF
Cytochrome C	rb	Santa Cruz	7159	1:1000	IB/IF
Erk	rb	Cell Signaling	9108	1:1000	IB

I κ B- α	rb	Cell Signaling	9242	1:1000	IB
Mcl-1	ms	Abcam	31948	1:1000	IB
Mek	rb	Santa Cruz	252	1:1000	IB
NF- κ B	rb	Santa Cruz	372	1:1000	IB/IF
PARP	rb	Santa Cruz	7150	1:1000	IB
p Akt	rb	Cell Signaling	4060	1:1000	IB
p Erk	ms	Cell Signaling	9106	1:1000	IB
p Mek	rb	Cell Signaling	2354	1:1000	IB
Puma	rb	Cell Signaling	4976	1:1000	IB
Sn	rb			1:50	IF
Tom40	rb	Santa Cruz	11414	1:500	IB

Table 2.9. List of Primary antibodies used for Immunoblotting (IB), Immunofluorescence(IF).

Secondary antibody	Source	Company	Dilution	Application
ECL anti-mouse IgG HRP linked	Goat/Donkey	GE healthcare	1:2500	IB
ECL anti-rabbit IgG HRP linked	Sheep /Donkey	GE healthcare	1:2500	IB
Anti mouse Cy2 linked	Goat	Dianova	1:200	IF
Anti rabbit Cy2 linked	Donkey	Dianova	1:200	IF

Table 2.10. Secondary Antibody used in the study.

2.1.10. Technical equipment

The following technical devices were used in this study

Hera Cell 150 incubator (Thermo), Hera Cell sterile bench (Thermo), Rotanta 460R centrifuge (Hettich), Avanti™ J-25I centrifuge (Beckman Coulter), cold centrifuge 5417R (Eppendorf), Owl Hep semidry electro-blotting system (Thermo), PerfectBlue™ Dual Gel Twin PAGE chambers (Pqrlab Biotechnology), DM1500 confocal microscope (Leica), confocal Leica TCS SP5, DMR epifluorescence microscope (Leica), DMIL light microscope (Leica), plate reader infinite M 200 (TECAN), Thermo-mixer comfort (Eppendorf), 2100 Bioanalyzer (Agilent Technologies), G –storm GS1 thermo cycler (GR1), Step One Plus RT PCR System (Applied Biosystems), Nano drop 1000 spectrophotometer (Pqrlab Biotechnology), ultra low temperature freezer (New Brunswick scientific), liquid Nitrogen tank (CBS 2300 series).

2.1.11. Software used

Windows XP, Microsoft Office 2007, EndNote X5, Adobe Photoshop CS4, Corel Draw X4, LAS-AF confocal microscopy software, ImageJ.

2.2. Methods

2.2.1. Cell culture

All cells were cultured in 75 cm² cell culture flasks (Greiner) in the corresponding medium as described above (see Table 2.3). The cells were maintained in a humidified incubator (Thermo) at 37 °C with 5 % CO₂. The cells were in culture only until ten passages. Trypsin-EDTA was used for splitting the cells upon confluence. The adherent epithelial cells were washed with sterile PBS (GIBCO, Invitrogen) once and detached by incubation with 1 ml Trypsin/EDTA (GIBCO, Invitrogen) per flask. Trypsinization was stopped after 3-5 minutes by re-suspending the cells in FCS containing medium. 10-20 % of cells were transferred into a fresh cellculture plate further cultured in fresh medium.

2.2.1a. Amoebal culture

Acanthamoeba castellanii, originally isolated as a cell culture contaminant was obtained from American Type Culture Collection (Mannasas, VA, USA). The amoebae were cultured axenically in peptone yeast glucose (PYG) medium at 25°C. Encystment was induced by washing the cells with phosphate buffer saline and incubating in encystment medium for 16h.

2.2.2. Cryo stocking of cell lines

For long term storage, and as the cells were maintained for no more than ten passages the same trypsinization procedure was performed to detach cells from cell culture plates, transferred to a 15 ml tube (Greiner) with 5 ml RPMI1640 + 10% FBS. After centrifugation at 800 rpm (Hettich) for 5 min, the cell pellet was resolved in 3 ml

stocking medium with 10% DMSO (cryoprotectant) and aliquoted into 1 ml per cryo tube, gradually cooled to -80°C in isopropanol after which the cryo tubes were transferred to liquid nitrogen tank where the temperature is -186°C. For thawing of cell stocks, frozen cells were rapidly thawed at 37 °C and immediately transferred into pre-warmed medium for re-culture. Cells are usually seeded in plates one night before performing experiments.

2.2.3. Infection with *Simkania negevensis*

The infection procedure was similar to as described above, but the media was 1x RPMI 1640+ L-Glutamax +25mM HEPES (GIBCO, Germany) with 10 % (v/v) heat inactivated FCS (Biochrom) and penicillin (100 U/ml), streptomycin (100 µg/ml), vancomycin (50 µg/ml), gentamycin (8 µg/ml) (to prevent any contamination). The media also contained cycloheximide (1 µg/ml); an effective inhibitor of protein biosynthesis in eukaryotes, at a lower concentration restricts the cell division. Since, Sn needs nearly 5 days to complete the life cycle at a MOI 1 the use of cycloheximide was inevitable.

2.2.4. Preparation of bacterial stocks

Owing to the obligate intracellular life style, *Chlamydiales* cannot be cultivated *in vitro* on solid or in liquid media. Therefore, infectious EB had to be prepared from infected cell cultures and stored as frozen stocks for later usage. In order to prepare a stock of *Simkania negevensis* Z, HeLa 229 or Hep-2 cells were seeded in a 75 cm² cell culture flask, infected at MOI 1, and incubated at 35°C and 5% CO₂ for 72 h, respectively. Infected cells were detached with a rubber policeman (Sarstedt) and

transferred to a falcon tube with sterile glass beads. Cells were ruptured by vortexing for 3 min and the supernatant containing chlamydial EB was transferred to twelve 150 cm² culture flasks of HeLa 229 or Hep-2 cells for propagation of infection in a dilution of 1:100. After 72 h of incubation, the cells were lysed as above. To remove cell debris, the suspension was centrifuged at 2,000 rpm for 10 min at 4°C (Hettich) followed by a centrifugation step at 25,000 x g for 1 h at 4°C (Beckman Coulter). The bacterial pellet was washed once with SPG (sucrose phosphate glucose) buffer, centrifuged as above, and resolved in 5 ml SPG buffer (Table 2.3). In order to separate clumps of bacterial EB, the bacterial suspension was passed through a 20 then 18 gauge needle for several times. The suspension was aliquoted and stored at -80°C. For each infection experiment, aliquots were freshly thawed and diluted in RPMI1640 + 5% FBS to reach the desired MOI.

2.2.5. Titration of bacterial stocks

To determine the appropriate amount of bacterial suspension to reach a MOI of 1 (one inclusion-forming unit (IFU) per cell) freshly prepared stocks of *Simkania negevensis* were titrated. Therefore HeLa 229 cells were seeded in 24-well plates on glass cover slips, the next day, were infected with different dilutions of the bacterial suspension, as described before. The cells were fixed after 72 hpi, with 4% PFA in PBS for 20 min at RT, washed twice with PBS and taken up for immunostaining. The cells were permeabilised with 0.2% Triton X 100 for 20 min. To prevent unspecific binding of the antibody the cells were incubated in 2% FBS in PBS for 1 h at RT then incubated with a mouse anti-chlamydial heat shock protein 60 (cHsp60) (1:500) or Sn

antibody (1:50) in 2% FBS/PBS for 1 h at RT. Cells were washed thrice with PBS and incubated with a secondary Cy2TM-linked sheep anti-mouse antibody in 2% FBS/PBS. To counterstain nuclei, cells were incubated with Hoechst 33342 dye (Sigma) (1:3000) for 30 min at RT, washed twice with PBS, and mounted with Mowiol mounting medium (Table 2.4). Bacterial inclusions and cellular nuclei were counted in an epifluorescence microscope (Leica) with 40x fold magnification to calculate the concentration of the stocks.

The MOI was calculated using the formula:

$$\text{IFU/ml} = \text{Number of inclusions in a 40X microscopic field} \times 1916.28 \times \text{dilution factor} \times 1$$

The factor 1 is used if 1 ml of the media is used and if 500 μ l is used the factor 2 is used for calculation MOI.

2.2.6. Apoptosis induction

To study if Sn could resist apoptotic, different apoptotic inducers like tumor necrosis factor α (TNF- α) applied together with cycloheximide (chx), required to prevent the survival pathway and staurosporine (STS) was used. After 3 dpi with Sn the media was removed and the cells were either treated with 20 ng/ml of TNF- α /3 μ g/ml of chx or 1 μ M of STS in 500 μ l fresh RPMI1640 + 5% FBS. These cells were incubated at 35°C for 4 h or 6 h respectively for TNF- α /chx and STS.

2.2.7. Assays to measure apoptosis

2.2.7.1. Hoechst or DRAQ5 staining

Following the indicated treatment, cells were stained with 20 μ M Hoechst 33258 or the far-red fluorescent DNA dye DRAQ5 at a dilution of 1:500 for 30 min at 37°C on glass slides. After fixing with 4% PFA, cells were stained and washed with PBS. Nuclear morphological changes (fragmentation or condensation) were determined under an epifluorescence microscope. At least 300 nuclei per sample were counted.

2.2.7.2. TUNEL assay

Fragmentation of chromosome by endonucleases is a hallmark of the later stage of apoptosis that results in a multitude of 3'-hydroxyl termini of DNA ends. This property can be used to identify apoptotic cells by labeling the DNA nicks with fluorescent-tagged deoxyuridine triphosphate nucleotides (F-dUTP). The enzyme terminal deoxynucleotidyl transferase (TdT) catalyzes a template-independent addition of deoxyribonucleoside triphosphates to the 3' hydroxyl ends of double- or single-stranded DNA and generates DNA strands with exposed 3'-hydroxyl ends. Addition of the deoxythymidine analog 5-bromo-2'-deoxyuridine 5'-triphosphate (BrdUTP) to the TdT reaction serves to label the break sites. Once incorporated into the DNA, an anti-BrdU antibody using standard immune histochemical techniques can detect BrdU. Non-apoptotic cells do not incorporate the F-dUTP because of absence of exposed 3'-hydroxyl DNA ends. Hence, to detect a significant difference in apoptosis of infected versus non-infected cells, DNA fragmentation was determined by the terminal deoxynucleotidyl transferase (TdT) mediated dUTP-2 nick endlabeling (TUNEL) method using the Dead EndTM Fluorometric TUNEL Kit (Promega). This method allows for detection of apoptotic cells on single cell level (Gavrieli et al, 1992). Therefore, cells were seeded on glass cover slips, infected or mockinfected, and

treated with TNF- α /chx for 4 h. Cells were fixed with 4% PFA for 20 min at 35°C and labeled according to the manufacturer's instructions. Briefly, cells were permeabilized with 0.2% [v/v] Triton X100 in PBS for 5 min, washed once with PBS, and stained with 1 μ g/ml Hoechst 33324 (1:3000) dye in PBS for 5 min. Cells were washed and permeabilized as above and equilibrated with equilibration buffer before incubation with the nucleotide mix and TdT enzyme for 1 h for 60 min at 37°C in a humidified chamber. The reaction was terminated with 2x SSC (saline sodium citrate). The cells were washed thrice and mounted with Mowiol. The ratio of TUNEL-positive cells was evaluated by counting five random fields in an epifluorescence microscope (Leica) with 40x fold magnification.

2.2.7.3. Luminescent caspases-8 activity assay

The autoprocessing of procaspase-8 into its active form is a prerequisite for the apoptotic actions of the initiator caspase (Kang et al, 2008). To determine the activity of caspase-8 in Sn-infected TNF- α /chx treated cells, a luminescence based Caspase-Glo-8 Assay (Promega) was performed. This assay makes use of a substrate with a LETD sequence that was proposed to be specifically cleaved by caspase-8 (Thornberry et al, 1997). According to the instructions, 15,000 HeLa 229 cells were seeded in a white flat bottom 96-well plate (Nunc) to reach about 70% confluency at the day of infection. Cells were treated as described above in a volume of 100 μ l and the luminescent caspase-8 substrate was added 4 h after TNF- α /chx induction. The plate was shaken for 30 sec at 450 rpm with a Thermomixer (Eppendorf) and incubated for 75 min at RT in the dark. Subsequently, luminescence was measured in a plate reader (Tecan) with light exposure duration of 1 sec/well.

2.2.7.4. Cytochrome c release

The cells were infected and treated with TNF- α /chx induction as described above. After 4 h of induction the cells were fixed with 4% PFA and taken up for immunostaining with cytochrome c antibody. The absence of cytochrome c in the mitochondria indicated a loss of membrane potential.

2.2.7.5. Active caspase-3 staining

The cells were infected and treated with TNF- α /chx induction as described above. After 4 h of induction the cells were fixed with 4% PFA and taken up for immunostaining with cleaved or active caspases-3 antibody. Uninfected cells induced with TNF- α /chx were taken as the positive control. Active Caspases-3 could be found on the surface of apoptotic cells.

2.2.7.6. Activation of Bax

The cells were infected and treated with TNF- α /chx induction as described above. After 4 h of induction the cells were fixed with 4% PFA and taken up for immunostaining with active Bax antibody. Uninfected cells induced with TNF- α /chx were taken as the positive control. Active Bax could be found accumulated on the mitochondria in apoptotic cells. The cells were analyzed under confocal microscope.

2.2.7.7. Heterodimerisation of Bax and Bak

Upon induction of apoptosis, Bax and Bak change their conformation and homo-oligomerize to permeabilize mitochondria (as described under 1.1.5.1.b). Hence it was necessary to investigate if Sn-infected cells upon apoptosis induction can prevent the oligomerisation of Bax and Bak. HeLa 229 cells were grown in 35 cm² plates to 60-70 % confluency. Apoptosis was induced as described above or mock

induced in the presence of 3 µg/ml cycloheximide. Supernatant was collected and the remaining cells were scraped with a rubber police and washed in PBS by centrifugation at 1,000 rpm for 3 min at 4°C. For mitochondrial isolation, the pellet was resuspended in Buffer A (20 mM Hepes pH 7.6, 220 mM mannitol, 70 mM sucrose, 1 mM EDTA, 0.5 mM PMSF and 2 mg/ml BSA) and left on ice for 15 min. Cells were homogenized 20 strokes with a homogenizer and pelleted at 800 g for 5 min at 4°C. Mitochondria containing supernatant was collected and centrifuged again at 10,000 g for 10 min at 4°C. Mitochondrial pellet was resuspended in Buffer B (Buffer A without BSA), quantified using a Nanodrop (Peglab, Germany) and stored at -80°C. Supernatant containing cytoplasmic proteins was kept in cytochrome c release assays. Mitochondria (60 µg) were pelleted (10,000 g, 10 min, 4°C) and washed once with SET-buffer (and resuspended in 95 µl SET-buffer. Cross-linking was done with BMH (Pierce, Rockford) at a final concentration of 1 mM for 30 min at RT. For quenching of the cross linker 2 µl DTT (2.5 mM) were added and samples were incubated for 5-10 min on ice. Cross-linked mitochondria were pelleted (14,000 rpm, 5 min, 4°C) and washed once in SET-buffer, resuspended in 30 µl Laemmli-buffer and analyzed by western blotting.

2.2.8. Infectivity assays

In order to investigate whether the production of simkianial progeny is altered by NF-κB activation, an infectivity assay was carried out. Therefore, bacterial inclusions were ruptured at the end of the developmental cycle and the particles were transferred to uninfected cells for a second round of infection. The primary infection is

described in section 2.2.3. At the end of the developmental cycle the inclusions were lysed by either incubating at -80°C for 1 h followed by incubation at 35°C and ruptured by pipetting the cells up and down or by glassbeads. Supernatant containing EB was transferred to freshly plated HeLa cells on glass cover slips in different dilutions. Infected cells were incubated for 72 h at 35°C and fixed in 4% PFA. Cells were stained for chlamydial Hsp60 and counterstained with Hoechst 33324 for DNA.

2.2.9. Inhibitor treatment

For inhibition of NF- κ B activation, cells were treated with 25 μ M Caffeic Acid Phenethyl Ester (CAPE) (Sigma) in DMSO in 500 μ l of medium. Stock solution of CAPE was made by dissolving CAPE in DMSO to make 25 mM, hence 1:1000 of stock (25 μ M) was used in each experiment. CAPE is a cell permeable active component of propolis from honeybee hives, a potent and specific inhibitor of NF- κ B activation. Control cells were treated with solvent alone. After 5 h of CAPE treatment the infected cells were induced with TNF- α /chx for apoptosis. This set up was also used for Sn for its effect on infection and infectivity.

To inhibit the PI3 kinase, a cell permeable, potent and specific phosphatidylinositol 3- kinase inhibitor LY294002 (Calbiochem) was used. It acts by binding to the ATP binding site of the enzyme. Stock solution of the inhibitor was made in DMSO. LY294002 was used at varying concentration of 0.1, 1 and 10 μ M and the controls were treated with the solvent alone to investigate the importance of this survival signal in apoptosis resistance.

2.2.10. Transfection

With the advent of RNA interference, the function of cellular proteins can be investigated by the delivery of small interfering RNAs (siRNAs) into the cells that then leads to the degradation of respective complementary mRNA transcripts (Elbashir et al, 2001). In order to deplete host cells of anti-apoptotic proteins, siRNA transfection was performed with LipofectamineTM 2000 (Invitrogen) or Polyethylenimine (PEI).

2.2.10.1. Polyethylenimine (PEI) transfection

Cells (70-80 % confluence) were seeded one day before in 24 well cell culture plates. On the next day, cells were washed with PBS and incubated in 5% FCS medium immediately before transfection. About 1 µg DNA was prepared in 100 µl Optimem transfection medium (GIBCO) for each sample and incubated at RT for 10 min after vortexing. In the meantime, 0.9 mg/ml PEI was prepared in 100 µl optimum (Table 2.3). PEI was reported to have higher efficiency in forming complexes with nucleic acids and was better delivered into the cells, PEI also have reduced toxicity as it reduces free polycations in the transfection media (Godbey et al, 1999). The samples were vortexed and incubated at RT for another 20 min. The mixture was eventually added to the cells for transfection. The cell culture medium was replaced after 4-6 h with normal medium containing 10 % FCS.

2.2.10.2. LipofectamineTM 2000 DNA delivery (Invitrogen)

In each transfection, the DNA (µg) and LipofectamineTM 2000 (µl) ratio was usually 1:2 to 1:3. One day before transfection, cells were seeded into 6-well plates to gain 70% confluency. 20 pM siRNAs were incubated in 200 µl Optimem transfection medium containing 4 µl LipofectamineTM 2000 for 25 min at RT before dropwise addition to 800 µl fresh RPMI medium containing 5% FBS. The media was removed

and replaced with 10% FCS media after 4-6 h. After 24 h post transfection, cells were infected with *Simkania* and experiments were performed as described before.

2.2.12. Microscopy

2.2.12.1. Leica Fluorescence microscopy

Nuclear fragmentation or condensation was detected by Leica DM RBE (Bensheim, Germany) fluorescence microscopy, following Hoechst staining as described in 2.2.7.1.

2.2.12.2. Confocal microscopy

Confocal microscopes from DM1500 (Leica) was used in this study. Cells growing on a cover slip were washed and fixed, following the indicated treatment. After fixation, cells were permeabilized with PBS containing 0.2 % Triton X 100 for 30 min. Before incubation with the primary antibody listed in Table 2.9 (1 h at RT), cells were blocked with 5 % FCS for 45 min. Cells were washed with PBS after incubation with the primary antibody, and further incubated with the corresponding secondary antibody (fluorescence conjugated) at RT for 1 h. Finally, cells were washed 3 times in PBS and once with distilled water to remove the PBS and mounted on a glass slide with Mowiol. Samples were kept at 4°C until analysis. Cells were inspected under laser scanning confocal microscope (Leica) with 60x fold magnification and an additional 1.5x software magnification. Images were further processed with the software Image J.

2.2.12.3. Electron microscopy (in collaboration with Prof. George Krohne)

The HeLa 229 cells were infected either with Ctr or with Sn for 24 h or 72 h respectively. The infected cells were washed twice with PBS solution and fixed with

gluteraldehyde at 4°C for 1 hr. The fixed cells were washed with cocodylate buffer and taken for preparation of the sample.

2.2.13. SDS-PAGE and Western blotting

Protein levels or post-translational modifications such as phosphorylation were detected using the sodium-dodecylsulfate polyacrylamide electrophoresis (SDS-PAGE). Gels of different density were prepared according to the table below. The proteins migrate in an electric field according to their size, which is mediated by SDS providing a uniform negative charge to the proteins. Different percentage of gels was used depending on the size of protein to be separated.

Solution components for Separating gel	6%	8%	10%	15%	Solution components for Stacking gel (5%)
H ₂ O	5.3	4.6	4.0	2.3	6.8
30% acrylamide mix	2.0	2.7	3.3	5.0	1.7
1.5M Tris (pH 8.8)	2.5	2.5	2.5	2.5	1.0 M Tris (pH6.8) 1.25
10% SDS	0.1	0.1	0.1	0.1	0.1
10% APS	0.1	0.1	0.1	0.1	0.1
TEMED	0.008	0.006	0.004	0.004	0.01

Table 2.11. Components of SDS PAGE.

Following the indicated treatment, the cells were transferred to ice, the medium with detached cells was collected, and the adherent cells were directly lysed in 100 μ l 2x Laemmli buffer. The lysates were then combined with the pellet of the respective detached cells after centrifugation at 4°C for 5 min at 350 x g and were heated to 95°C for 5 min. For phosphoproteins, lysis buffer containing phosphatase inhibitors was used (see Table 2.5) pipetting up and down, and transferred to a reaction tube (Eppendorf). Cell debris was removed by centrifugation for 5 min at 13,000g and 4°C. The supernatant was transferred to a fresh tube and mixed with an equal volume of 2x Laemmli buffer. Lysates were heated to 95°C for 5 min and stored at -20°C until used. Denatured protein lysates were loaded onto the gels, besides the pre stained protein ladder (Fermentas, #SM0671). Gels were subjected to 80 volts for about 10-15 min until the proteins move into the separating gel, followed by a complete run at 120 volts for about 45-50 min. Subsequently, proteins were transferred to a methanol activated PVDF membrane (GE Healthcare) in a semidry electro blotting system (Thermo) with a current of 1.0 mA per cm² membrane for 2 h. Membranes were rinsed in TBST₂₀ (See Table 2.4) for 1 min before blocking the membrane for 1 h in blocking buffer to reduce unspecific binding of the antibody. The membrane was incubated with the respective primary antibodies listed in table 2.9, overnight at 4°C. After washing the membrane thrice for 10 min in TBST₂₀, antibody-antigen complexes were detected by respective HRP-linked donkey anti- rabbit or sheep anti-mouse secondary antibodies (GE Healthcare) listed in table 2.10. Further the blot was washed thrice 10 min each in TBST₂₀ before developing in the x-ray film (Konika Minolta) or in the developing machine (ChemoCam Imager INTAS). For re-

probing with other antibodies, membranes were re-activated with 100% methanol and incubated in stripping buffer (Table 2.3) for 30 min at RT, after which the membrane was blocked for 1 h and then taken up for primary and secondary antibody for detection (as described above).

2.2.14. EMSA (in collaboration with Dr. Bhupesh K Prusty)

HeLa 229 cells were infected with Sn from day 1 to day 5; the infected cells with control were taken up for electro mobility shift assay. The cells were treated with ice cold hypotonic buffer containing (20 mM HEPES, 20% glycerol, 10 mM NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 1 mM DTT, 0.1% Triton X-100, 100 mM PMSF and cocktail of protease inhibitors). After 15 min incubation in ice, the lysates were centrifuged at 850g for 15 min at 4°C. The supernatant which contain the cytoplasmic extract was removed and the pellet was washed with hypotonic buffer and treated with 2.5 times the pellet size of nuclear extraction buffer (20 mM HEPES, 25% glycerol, 500 mM NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 1 mM DTT, 0.1% Triton X-100, 100 mM PMSF and cocktail of protease inhibitors) after 1 h the extraction mixture was centrifuged at 18000g for 15 min at 4°C. The supernatant was stored at -80°C. The oligo nucleotides described in materials were annealed and labeled with (γ^{32} P) ATP by T4 polynucleotide kinase and gel purified in 15% polyacrylamide gel. The binding reaction was performed in a 25 μ l reaction mixture containing 50% glycerol, 60 mM HEPES, 20 mM HCl, 300 mM KCl, 5 mM EDTA, 5 mM DTT, 100 μ g of BSA/ml, 2.5 μ g of (poly dl-dC) and 10 μ g of nuclear extract. After 5 min, 10,000 cpm of (γ^{32} P) ATP 5' end labeled double stranded oligonucleotide probe was incubated for 25 min at RT.

The DNA protein complex was resolved in 4.5% non-denaturing PAGE dried and exposed to X-ray films.

2.2.15. RNA Isolation

RNA isolation was performed for quantification of specific transcripts by quantitative reverse transcription polymerase chain reaction (qRT-PCR). HeLa cells in 6-well plates were infected with Sn from day 1 to day 5. Cells were lysed in 1 ml TRIzol reagent (Invitrogen) per 6-well, transferred to reaction tubes (Eppendorf) and incubated for 5 min at RT. After addition of 0.2 ml chloroform, the samples were shaken, incubated for 5 min at RT, and centrifuged at 12,000g for 15 min at 4°C to separate RNA from DNA and proteins. The upper, aqueous phase containing RNA was transferred to a fresh tube and treated with 0.5 ml isopropyl alcohol to precipitate the RNA. Samples were incubated for 10 min at RT and centrifuged for 10 min as above. The RNA pellet was washed once with 1 ml 75% ethanol and centrifuged at 7,500g for 5 min. The RNA pellet was air dried, dissolved in 50 µl DEPC H₂O, and stored at -80°C until further use.

2.2.16. DNA digestion

In order to remove contaminating DNA from isolated RNA, DNA was digested with the TURBO DNaseTM Kit (Ambion). 5 µl TURBO DNase buffer and 1 µl DNase were added to 50 µl RNA sample and incubated at 37°C for 20 min. After addition of 5 µl inactivation reagent, samples were mixed, incubated at RT for 5 min, and centrifuged at 10,000g for 15 min. The supernatant was transferred to a fresh reaction tube.

2.2.17. Copy (c) DNA synthesis

For qRT-PCR, isolated mRNA was reverse transcribed into copy DNA (cDNA) with the Superscript VILO™ cDNA Synthesis Kit (Invitrogen) according to the manufacturer's instructions. 4 µl 5 x VILO Reaction Mix and 2 µl enzyme Mix was added to 2 µg RNA and DEPC-H₂O in a total volume of 20 µl. Reverse transcription into cDNA was performed in a thermocycler (GRI) with the following temperature profile: 10 min at 25°C, 60 min at 42°C, and 5 min at 85°C. Samples were stored at -20°C until further use.

2.2.18. Quantitative reverse transcription polymerase chain reaction (qRT-PCR)

To quantify the amount of specific mRNA populations, qRT-PCR was performed. Amplification of cDNA and quantification of amplicates were performed in a Step One Plus RT PCR system (Applied Biosystems) using ABSolute Blue QPCR SYBR low ROX mix (Thermo) according to the manufacturer's protocol: 0.1 µl of cDNA was mixed with 10 µl 2x ABSolute Blue QPCR SYBR low ROX mix, 125 nM of each primer (table 2.3), and ddH₂O was added to a total volume of 20 µl. Each sample was analysed in triplicates.

2.2.19. Statistical analysis

Statistical significance of the acquired data was calculated with the two-sided Student's T test.

3. Results

3.1. Establishing *S negevensis* infection in cell cultures

S. negevensis strain Z was obtained from ATCC (ATCC VR-1471^T). The bacterium was cultivated as explained in the methods (2.2.3) and was titrated as explained in (2.2.4). HeLa 229 cells were plated in 12 well dishes with glass slides and were infected with Sn at a MOI of 1. After 72 hpi the cells were observed under light microscope. The cells were filled with tar like patches mostly in the perinuclear region in the cytoplasm. With increasing time of infection these patches extended and occupied a large proportion of the cytoplasm. At later time, some so called 'inclusions' looked empty, however when observed under phase contrast microscope fine rapidly moving particles could be observed. The cells were attached and still harbored the bacteria until 5 dpi, after which the cells were lysed and the bacterial particles were released into the medium. At a lower MOI the infection could proceed to nearly 8 days until the cells lysed as observed by (Kahane et al, 2002). The cells in later stages of infection looked more flat and expanded in morphology. It was also noticable that they stopped dividing as soon as they were infected and a visible inclusion could be seen. An electron microscopy of the Sn infected cells is shown in Figure 3.1b. All the cells that were tested were infectable with Sn (Figure 3.1a).

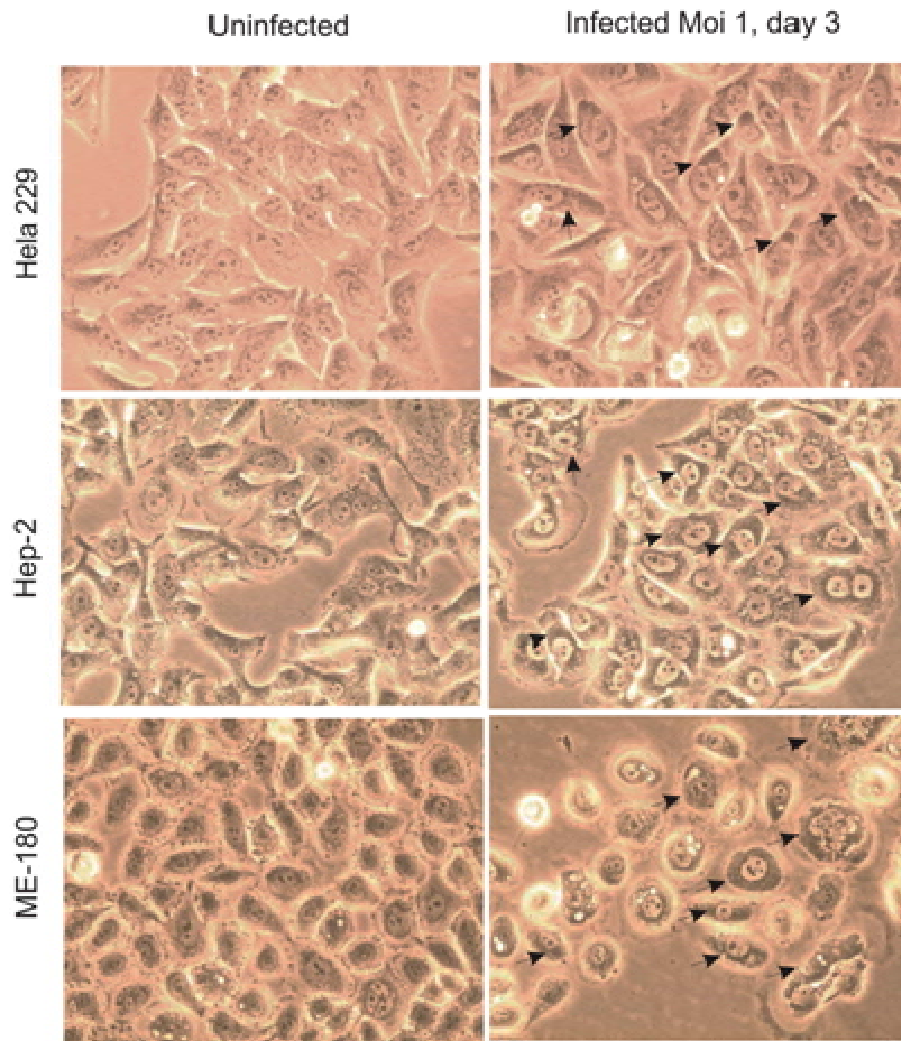


Figure 3.1a. Different cell lines like HeLa 229, HEp-2 and ME-180 were tested for Sn infection. Phase contrast images were taken after 3 dpi. The dark tar like patches in the peri-nuclear region of the cells indicates the Sn inclusions (indicated by arrows).

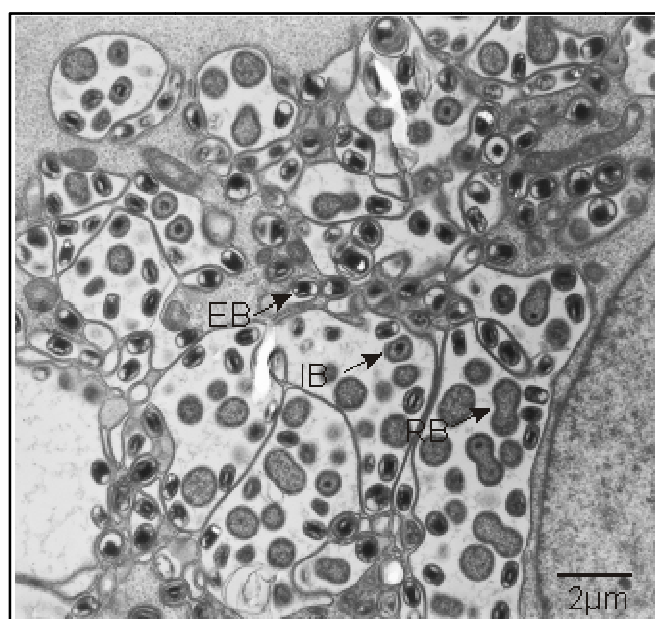


Figure 3.1b. Transmission electron micrograph of Sn in membranous inclusion of an infected cervical cancer cell. Black arrowheads indicate rod-shaped mature elementary bodies (EB), dividing spherical reticulate bodies (RB) and intermediate bodies (IB). Bar 2 μ m

3.2. *S. negevensis* infected cells are resistant to apoptosis

Apoptosis resistance is a hallmark of *Chlamydia* infection but has so far not been investigated for other family level related bacteria like *Simkania negevensis*. To test whether *Simkania* confers apoptosis resistance during infection, apoptosis was induced with human tumor necrosis factor alpha (TNF- α) in the presence of cycloheximide (TNF- α /chx) in infected and non-infected HeLa cells. The cells were fixed and stained with Hoechst to detect chromatin condensation (Figure 3.2a).

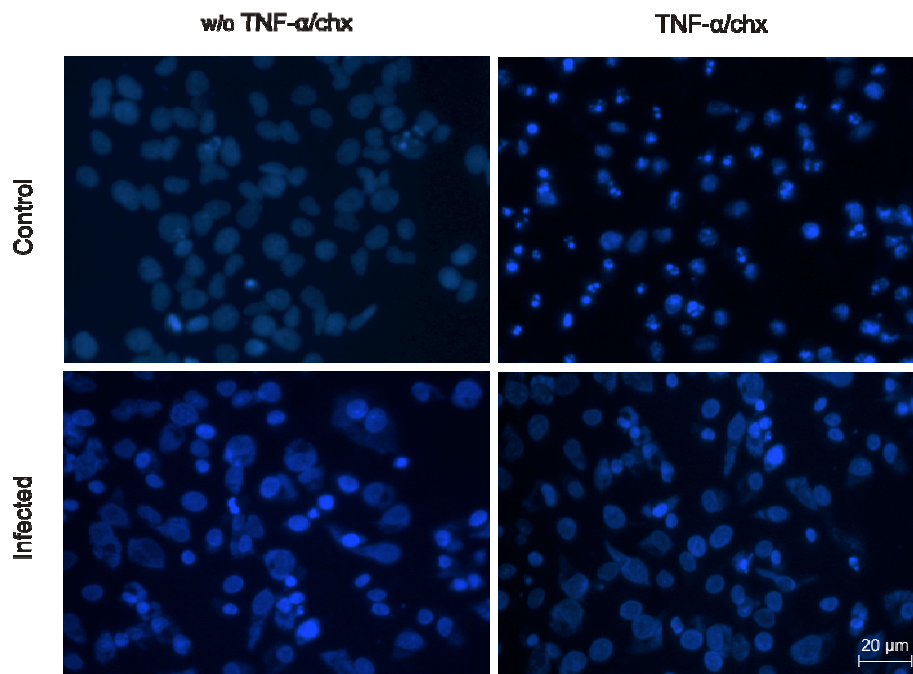


Figure 3.2a. HeLa 229 was infected with Sn for 72 h. The control and infected cells were treated with 20 ng/ml of TNF- α and 3 μ g/ml of chx in 5% FCS media for 4 h, after which the cells were fixed with 4% PFA and stained with Hoechst or Draq5 and analysed under confocal microscope. The total

number of cells and apoptotic cells were counted and the percentage of apoptotic cells were calculated by dividing the total number of apoptotic cells by the total number of cells. Bar 20 μ m. n=3.

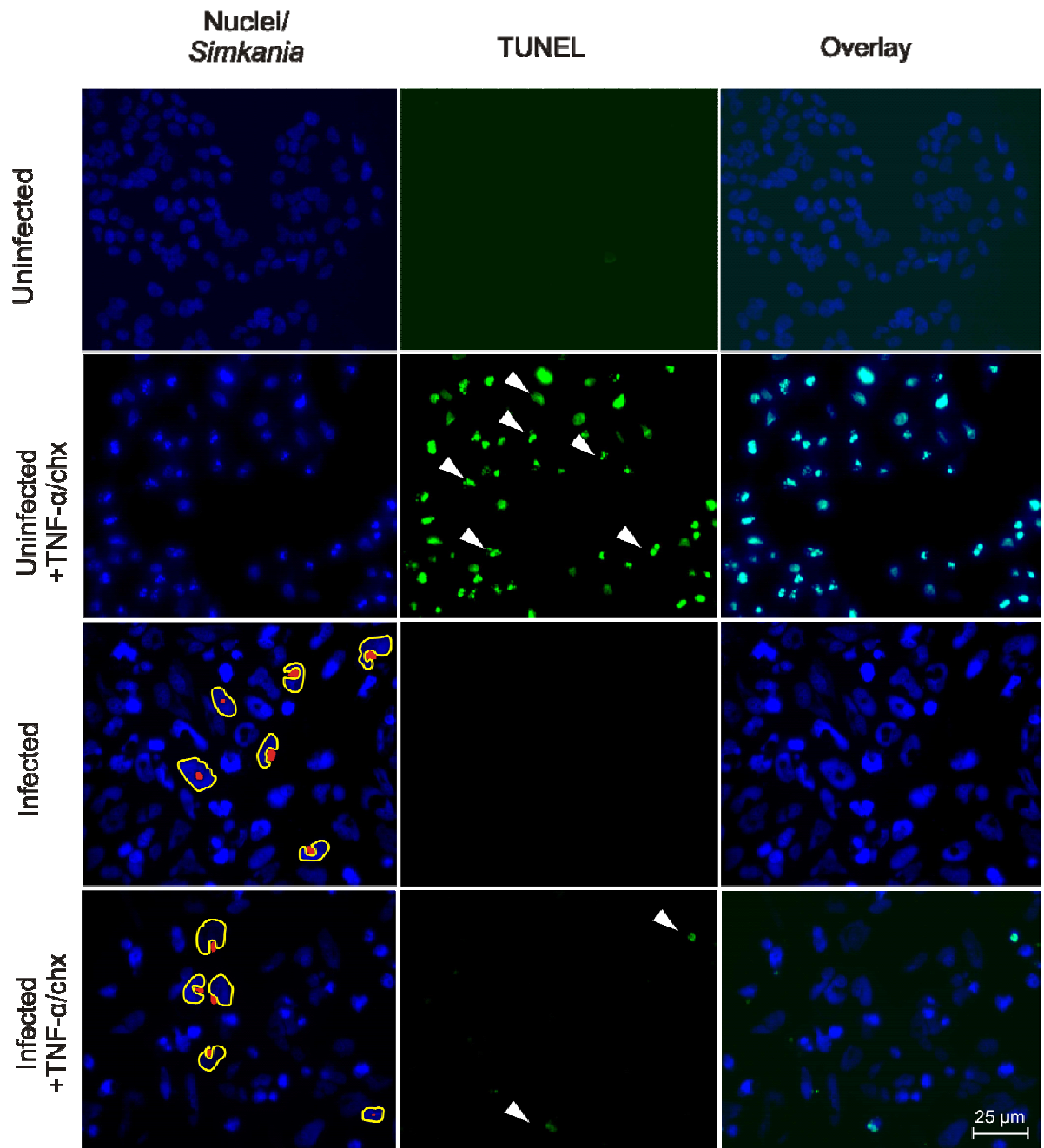


Figure 3.2b. *Simkania negevensis* infected HeLa cells are resistant to apoptosis induced by TNF- α . HeLa cells with or without *Simkania* infection (MOI 1) were treated with 20 ng/ml TNF- α with 3 μ g/ml chx or with carrier for 4 h. Samples were stained with Hoechst (blue) and TUNEL (green) and viewed under a epifluorescence microscope. Bar 25 μ m. (n=2).

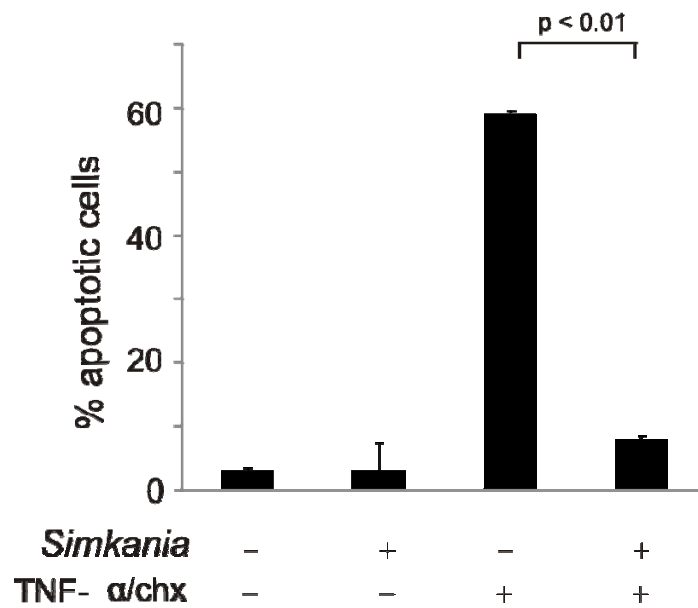


Figure 3.2c. Bar diagram displaying the quantitative analysis of the experiment shown in Figure 3.2b. Cells from five random fields were counted under a 40x objective and the percentage of apoptotic cells was calculated. *Simkania* infection significantly decreased the number of apoptotic cells upon TNF- α stimulation to nearly background levels (n = 2).

In a similar experiment apoptotic cells were quantified by terminal transferase mediated dUTP nick end labeling (TUNEL) assay (Figure 3.2b). A nearly complete block of apoptosis induced by TNF- α was observed at day 3 dpi illustrated by a reduction in the number of apoptotic cells from ~60% to ~10% in infected cells (Figure 3.2c). These results suggested an anti-apoptotic activity in cells infected with *Simkania*.

3.3. Sn resists apoptosis in a time and MOI dependent manner

To investigate if the resistance to apoptosis in Sn-infected cells depends on the establishment of the inclusion in the cells and the number of EB infecting the cell, time frame infections were carried on. Two conditions were considered under study. In the first case HeLa 229 cell were plated on glass slides and infected with different

MOI of Sn ranging from 0.5 to 20 for 72 h and the cells were induced for apoptosis using TNF- α /chx for 4 h. The cells were fixed and stained as described before (3.2) and the percentage of apoptotic cells was calculated for analysis. Results are shown in Figure 3.3a. In the second case HeLa 229 cells were infected with Sn at a MOI of 1 and apoptosis was induced after different time points i.e., day 1, 3 and 5. Percentage of apoptotic cells were calculated and analysed (Figure 3.3b).

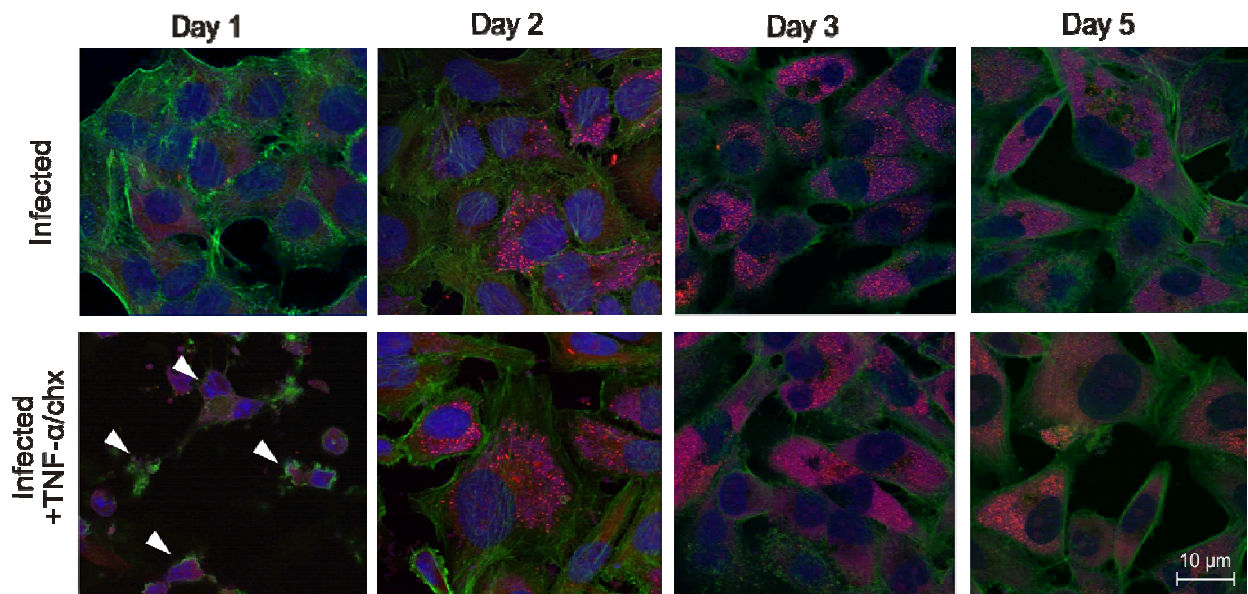


Figure 3.3a. Immunofluorescence analysis of the time and dose dependency of *Simkania*-mediated anti-apoptosis. HeLa cells were infected with *Simkania* for 1–5 days, MOI 0.5, 5.0, 10 and 20, induced with 20 ng/ml TNF- α /3 μ g/ml chx or with carrier for 4 h and stained with Draq5 (nuclei+inclusions, blue), Syto 82 (accumulates in *Simkania*, red) and Phalloidin (actin, green). Images shown are from an experiment with MOI 0.5; MOI 5, 10 and 20 are not shown. Infection led to apoptosis resistance from day 1 on. Bar-10 μ m, n = 3

Time course experiments showed time-dependent resistance for TNF- α /Chx-induced apoptosis at a multiplicity of infection of 0.5 beginning at 1 dpi and was similar to non-treated cells at day 3 with <10% apoptotic cells (Figure 3.3c). Further,

apoptosis resistance was found to be dependent on the MOI, cells infected with higher MOI acquired apoptosis resistance much faster as demonstrated in a quantification of TNF- α /chx-induced apoptosis at day 1 using MOI ranging from 0.5 to 20 (Figure 3.3c).

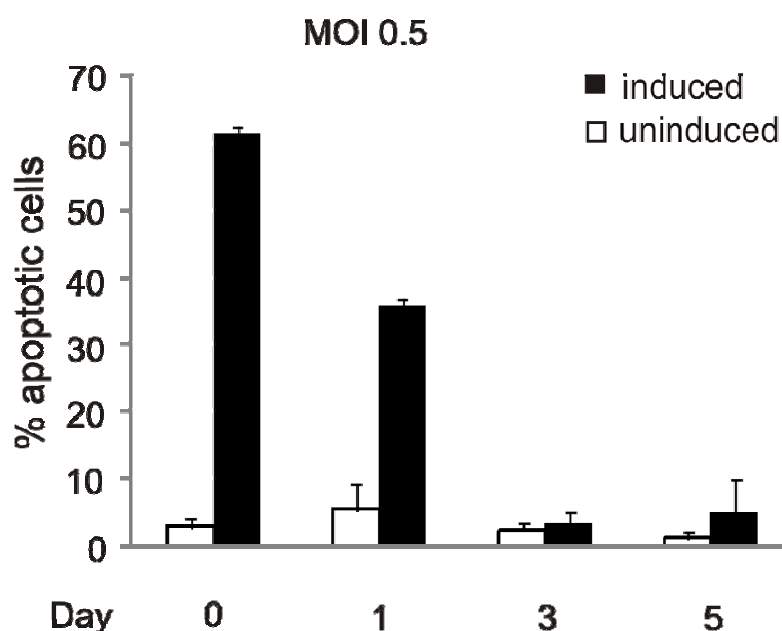


Figure 3.3b. Bar diagram displaying the quantitative analysis of the time dependency at MOI 0.5 from the experiment show in Figure 3.3a. Cells from five random fields were counted under a 40X objective and the percentage of apoptotic cells was calculated. Apoptosis resistance increased till day 3; towards the end of the infection cycle apoptosis sensitivity slightly increased until day 5. At higher MOI infected cells became more susceptible to apoptosis towards end cycle. n = 3.

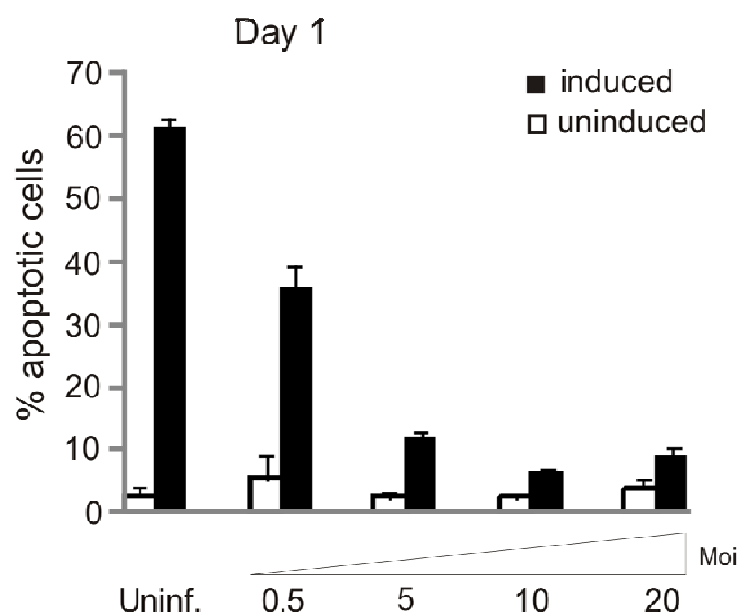


Figure 3.3c. Bar diagram displaying the quantitative analysis of the MOI dependency at day 1. Apoptosis resistance was found to be clearly dose dependent, increasing to MOI 10. At MOI 20 increased apoptosis sensitivity was observed. $n = 3$.

3.4. Sn infected cells resist apoptosis induced by Staurosporine

To test whether the intrinsic apoptosis pathway is inhibited, *Simkania*-infected cells were treated with the broad range kinase inhibitor staurosporine (STS). HeLa 229 cells were plated and infected with Sn at a MOI of 1 for 3 days and induced with 1 μ M STS for 5 h. After the treatment the cells were fixed and stained as described before. And the percentage of apoptotic cells was calculated. Infection reduced the apoptotic population in STS-treated cells in the same manner as observed in TNF- α /chx-treated cells (Figure 3.4). Taken together, *S. negevensis* inhibits both TNF- α /chx and STS-induced apoptosis in a time and infection dose-dependent manner

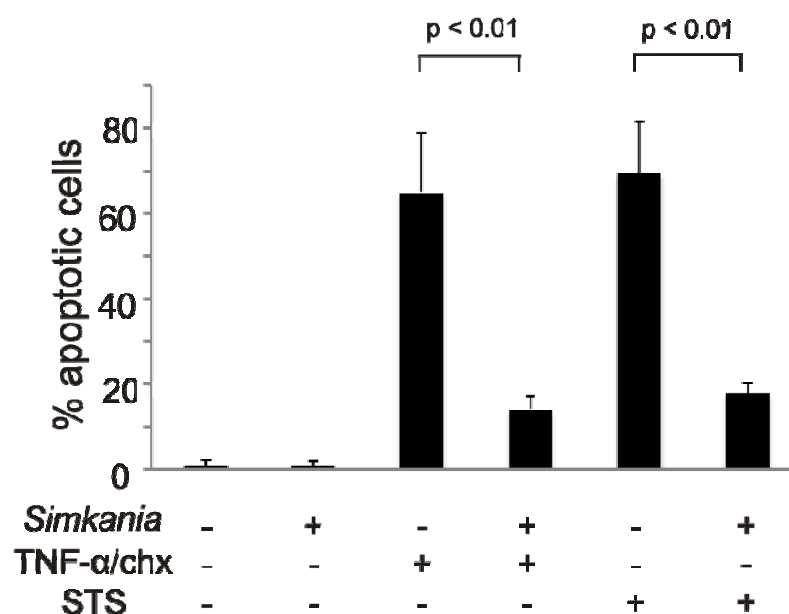


Figure 3.4. Bar diagram displaying the quantitative analysis of an infection/apoptosis induction experiment using either TNF- α /chx or STS. HeLa cells with or without *Simkania* infection (MOI 0.5) were treated with 20 ng/ml TNF- α /3 μ g/ml chx, STS 1 μ g/ml or with carrier for 4 h. Samples were stained with Hoechst 33258 (images not shown), five random fields were counted under a 40x objective and percentage of apoptotic cells was calculated. *Simkania* infection significantly decreased the number of apoptotic cells upon TNF- α /chx or STS stimulation, (n = 2).

3.5. TNFR is not shed during Sn infection

Chlamydia trachomatis infection differentially regulates the surface expression of TNFR1 and TNFR2 on the cell surface (Paland et al, 2008). TNFR is produced as a membrane anchored protein whose extra cellular domain can be released by proteolysis, a process called protein ectodomain shedding. In the case of TNFR this process is mediated by TNF- α converting enzyme (TACE) (Black et al, 1997). Upon *Chlamydia* infection, the bactericidal action of secreted TNF- α (a major weapon of immune system) is regulated by the activation of TACE and shedding of

TNFR from the cell surface (Paland et al, 2008). This could also explain one of the mechanisms by which *Chlamydia* resist apoptosis induced by TNF- α . As Sn was also found to resist apoptosis induced by TNF- α , curiosity raised the question if TNF- α binds to TNFR, and signals the survival pathway. Hence HeLa cells were plated and infected with Sn for 72 h and induced with TNF- α in the absence of chx for different time points ranging from 5 min to 60 min. The cell lysate was taken up for western blots (as described in Methods 2.2.13). MEK and ERK were phosphorylated in Sn infected cells as well as the uninfected cells, which indicated that Sn activates survival pathway that may serve to complete its life cycle (Figure 3.5). This also indicated that Sn infected cells have intact TNFR1 on cell surface and they have normal TNFR1 signaling upon TNF- α induction.

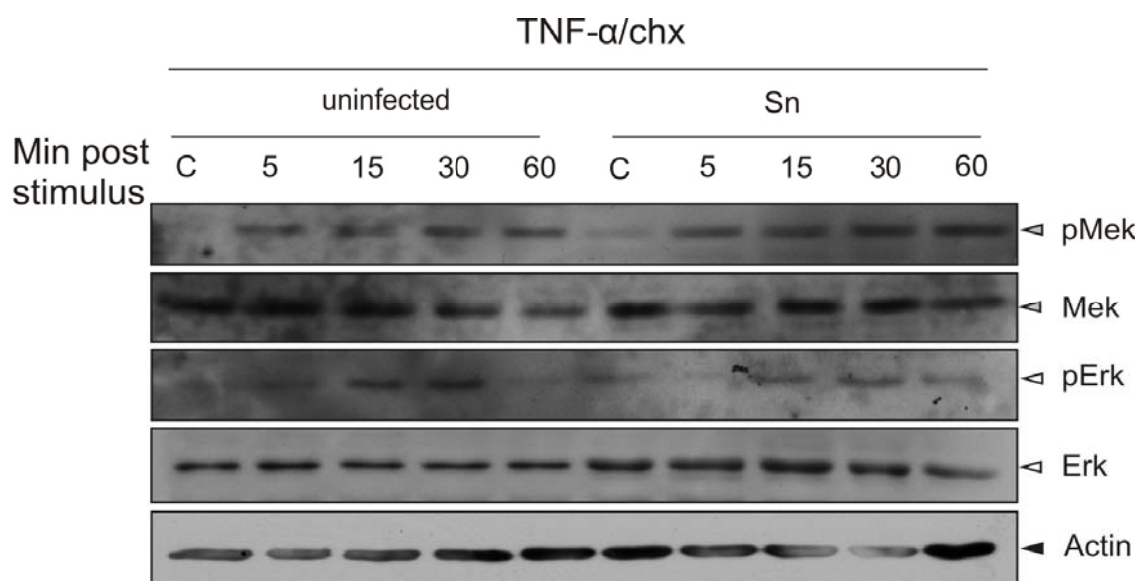


Figure 3.5. TNF receptor is activated in *Simkania* infected cells. HeLa cells with or without *Simkania* infection (MOI 1) were treated with 20 ng/ml TNF- α without chx for 5, 15, 30 and 60 min to activate the MEK-ERK pathway. The figure shows the phosphorylation of MEK (grey arrowheads) and ERK (white arrowheads), indicating that the TNF receptor is active. Actin is used as the loading control. n = 2.

3.6. Caspase maturation is differentially regulated in *Simkania*-infected cells

TNF- α -induced apoptosis depends on a well characterized signaling cascade (Wallach et al, 1999b) and is thus suited to more precisely define the block in apoptotic signaling in *Simkania*-infected cells. To investigate whether *Simkania* blocks the proteolytic cleavage and activation of caspases, infected and TNF- α /chx treated cells were tested for caspase processing and activity. Both caspase-3 cleavage and activity were inhibited by *Simkania* infection (Figure 3.6a and 3.6b). The treated and infected cells were also taken up for immunostaining, and the percentage of apoptosis was counted under the confocal microscope. This revealed the infected cells showed only ~11 % of activated caspase-3 against ~35 % of the uninfected induced cells (Figure 3.6c). Caspase-3 cleavage leads to proteolytic degradation of key proteins such as the nuclear enzyme poly-ADP ribose polymerase (PARP). PARP degradation was inhibited in *Simkania*-infected TNF- α /chx-induced cells (Figure 3.6a), confirming a strongly reduced caspase-3 activity in infected cells.

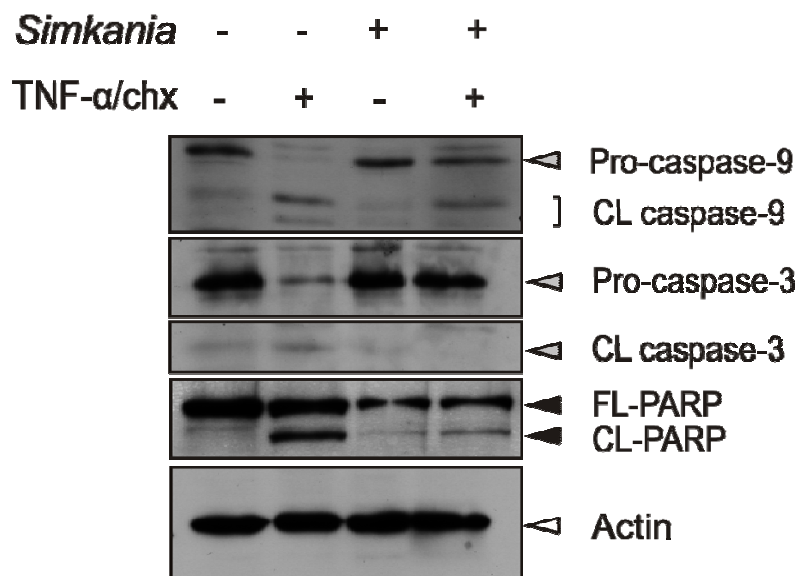


Figure 3.6a. HeLa cells with or without Sn infection (MOI 0.5, 3 days) were treated with 20 ng/ml TNF- α /3 μ g/ml chx for 4 h before analysis. Immunoblot showing the activation status of caspases-3, -8 and -9 (grey arrowheads) as well as PARP (black arrowheads) cleavage. Caspase-9 and -3 were not found to be cleaved in infected cells compared to uninfected induced cells. PARP is also not cleaved nor activated on induction in Sn-infected cells. Actin (white arrowhead) is used as the loading control. n=2

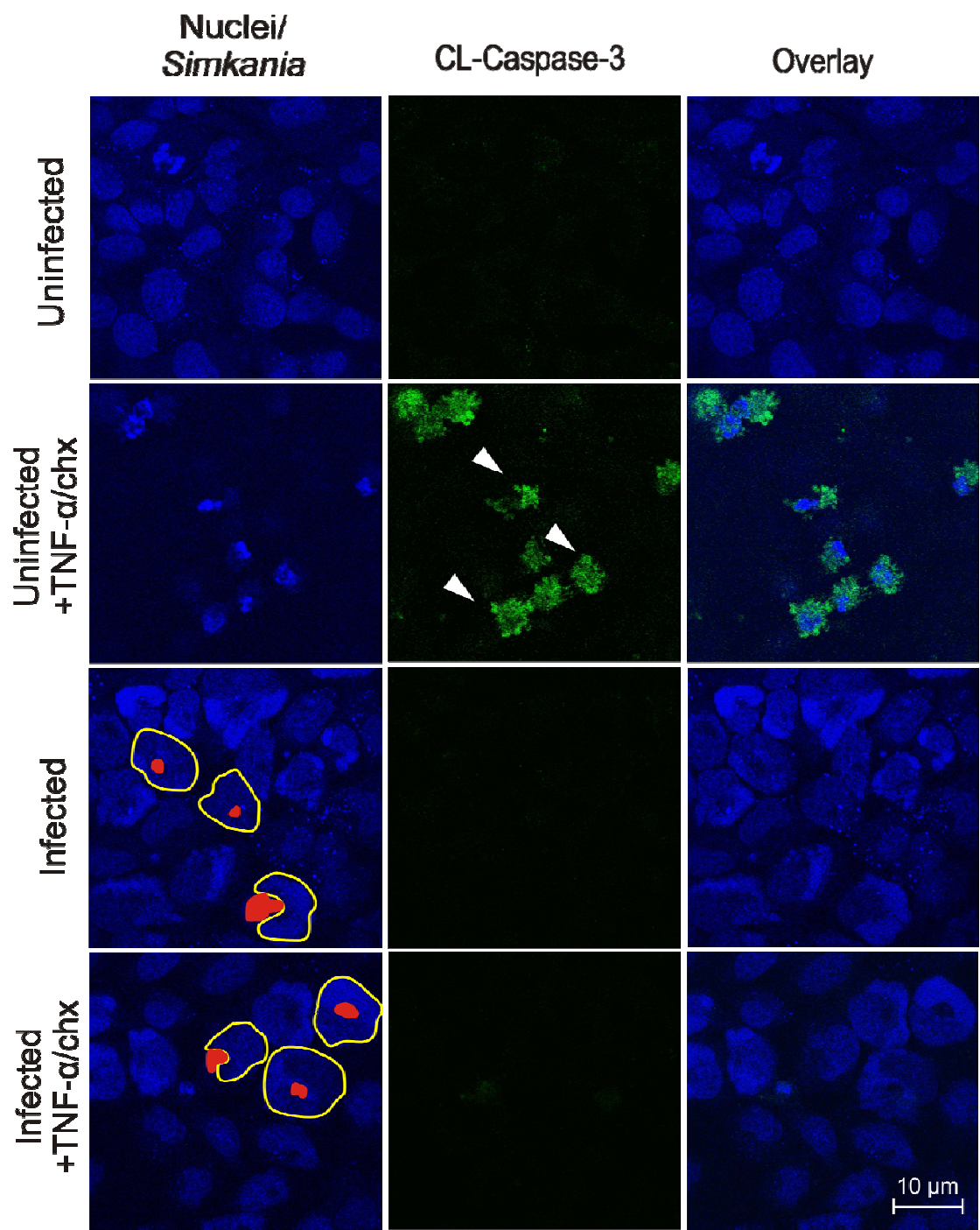


Figure 3.6b. Immunofluorescence analysis showing that caspase-3 is not activated in Sn-infected cells on induction with TNF- α /chx. Nuclei and bacteria were stained with Draq5 (blue) and activated caspase-3 was detected with an antibody specific for the cleaved protease (green, CL-Caspase 3). White arrowheads mark active caspase-3. Bacterial inclusions are exemplified by yellow open and nuclei by red filled circles. Bar-10 μ m, n = 2.

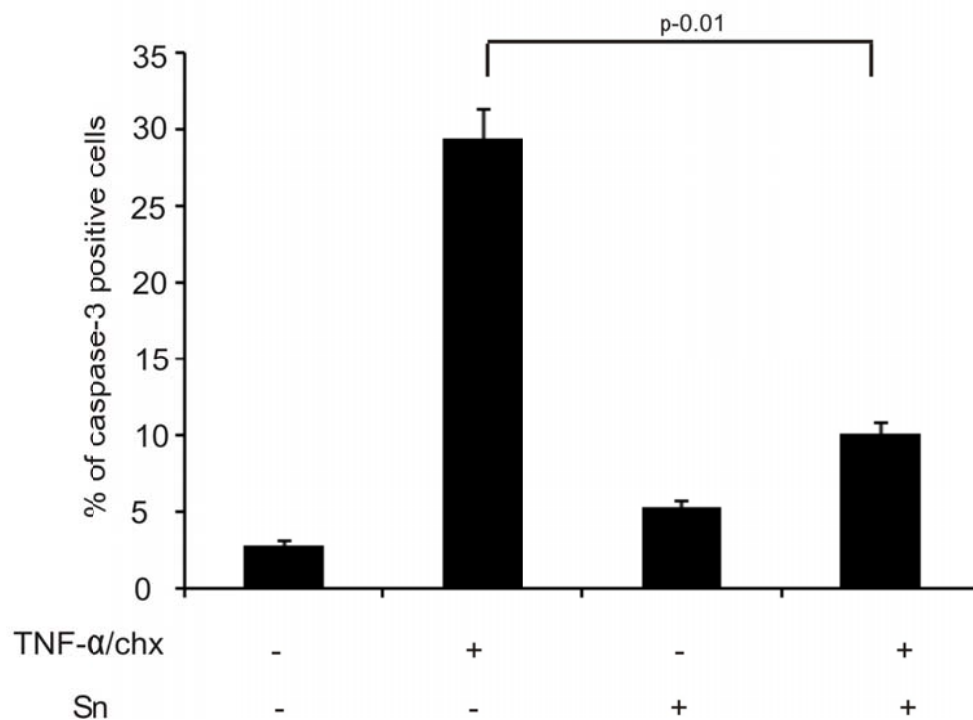


Figure 3.6c. Bar diagram displaying the quantitative analysis of the caspase-3 activation at MOI 0.5 from the experiment shown in Figure 3.6b. Cells from five random fields were counted under a 40x objective and the percentage of caspase-3 positive cells was calculated. *Simkania*-infection strongly reduced caspase-3 activation. n = 3.

To investigate if Sn-infection affects caspase-9 and caspase-8, processing or activity of the respective Caspases were tested. Interestingly, while caspase-9 processing was blocked, caspase-8 activity was not affected by infection with *Simkania* (Fig. 3.6a and 3.6d), demonstrating the selective inhibition of caspases in

cells infected with *Simkania*. Rather, Sn infections lead to the activation of caspase 8 even without apoptosis induction.

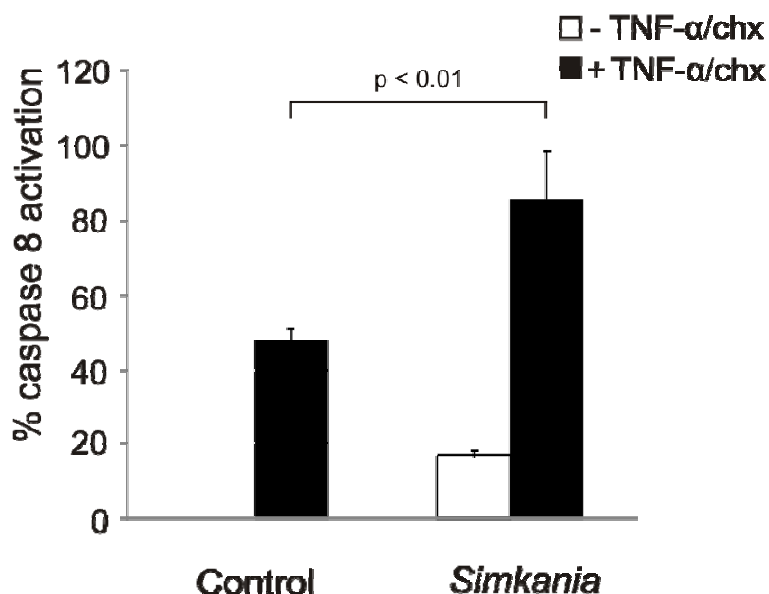


Figure 3.6d. Bar diagram showing the result of a caspase-8 activity assay (caspase-8 glo). Activation of caspase-8 is not blocked by Sn infection. n = 3.

3.7. *Simkania* infection inhibits apoptosis on the upstream of mitochondria.

Block of caspase-9/-3 in the presence of active caspase-8 is indicative of an apoptosis inhibition at or upstream of the mitochondria (Lakhani et al, 2006). When the cell death pathway is activated, activation and heterodimerisation of various pro-apoptotic proteins lead to the mitochondrial membrane potential loss. Mitochondrial cytochrome *c* is translocated to the cytosol of cells undergoing apoptosis where it participates in caspase-9 activation (Kluck et al, 1997). Hence, it was tested if Sn infection can prevent cytochrome *c* release from the cells treated with TNF- α /chx induction. While TNF- α /chx treatment induced the release of cytochrome *c* from mitochondria of uninfected cells, this was not the case in *Simkania*-infected cells (Fig.

3.7a, 3.7b). Failure to release cytochrome *c* indicated incomplete activation of Bax and/or Bak upon apoptosis induction. Bax, once activated undergoes a conformational change permitting insertion into the mitochondrial membranes. First, it was excluded that either Bax or Bak are differentially transcribed during infection (data not shown). Then whether Bax translocation into mitochondria is affected in Sn-infected cells upon TNF- α /chx -induced apoptosis was tested. Immunostaining confirmed strongly reduced levels of translocated Bax in infected cells upon apoptosis induction (Fig. 3.7d). Once activated Bax and Bak form oligomers in the mitochondrial outer membrane leading to the release of pro-apoptotic factors like cytochrome *c*. Bax and Bak oligomerisation was done via mitochondria isolation and *in vitro* cross-linking using BMH (as described in methods 2.2.7.7). Neither Bax nor Bak were found to form oligomers after TNF- α /chx treatment in *Simkania*-infected cells in comparison to non-infected cells (Fig. 3.7c). Thus, *Simkania* infection inhibits Bax translocation to the mitochondria as well as Bax/Bak oligomerisation.

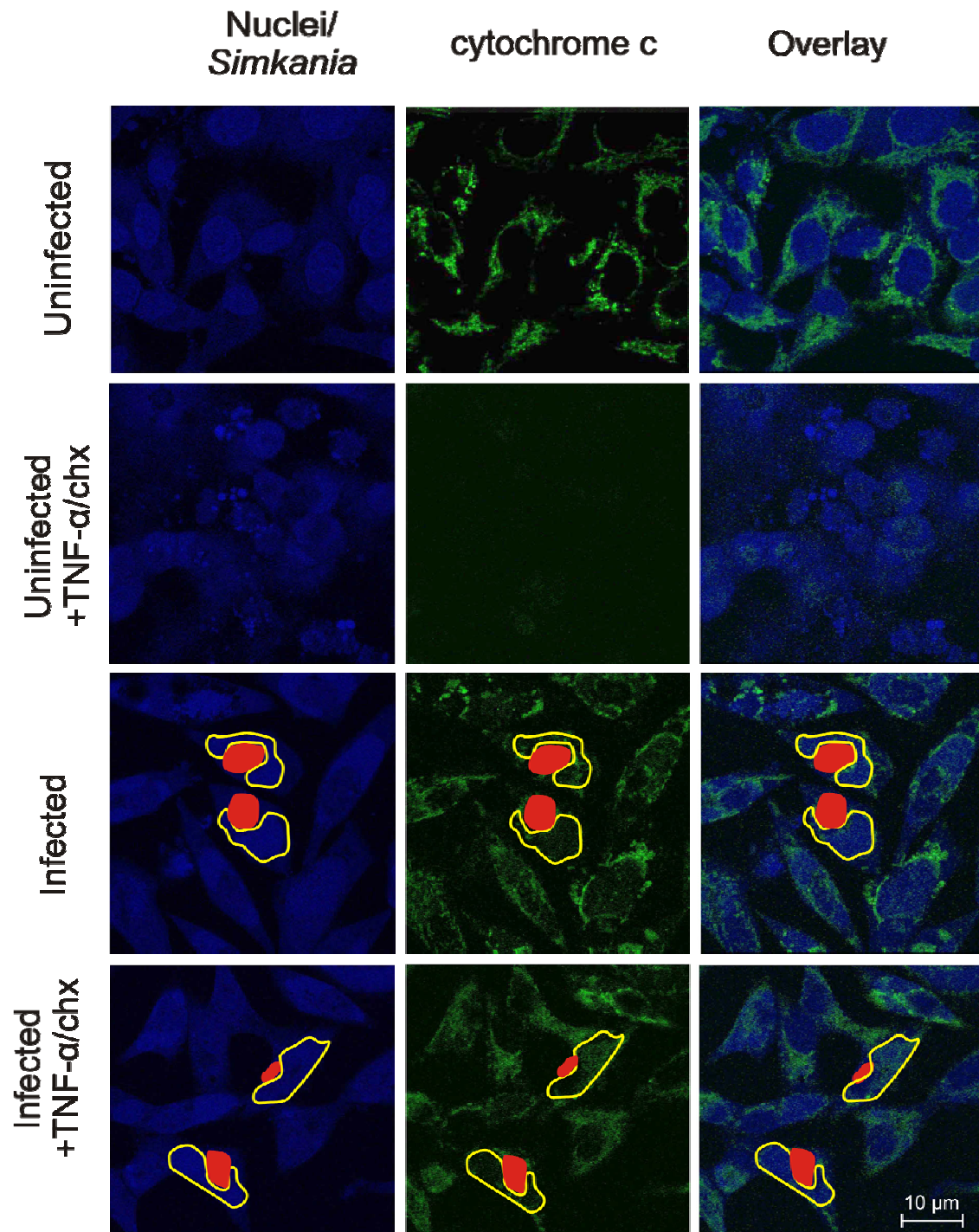


Figure 3.7a. Immunofluorescence staining on the cytochrome c distribution after *Simkania* infection on HeLa cells with or without *Simkania* infection (MOI 1, 3 days) were treated with 20 ng/ml TNF- α /3 μ g/ml chx or carrier for 4 h before analysis. Cells were stained for cytochrome c (green), *Simkania*/nuclei (blue) and viewed with a confocal microscope. Upon apoptosis induction cytochrome c is released from the mitochondria (uninfected+TNF- α /chx), this was not the case for infected cells (infected+TNF- α /chx). Bar- 10 μ m.

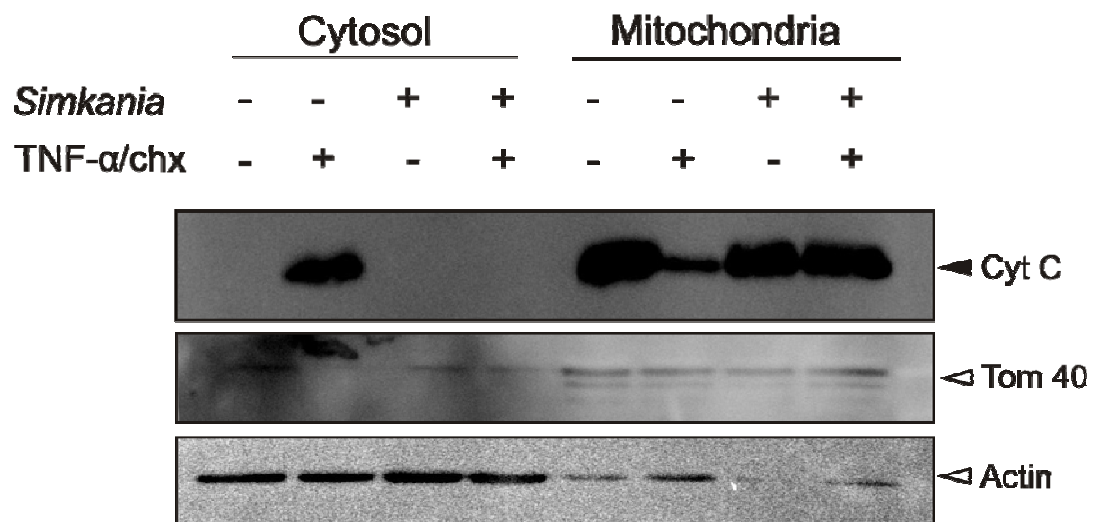


Figure 3.7b. Western blot analysis for cytochrome c release. Cytosol and mitochondria were isolated as described in the experimental procedures section and cytochrome c was detected by Western blot. cytochrome c release was completely blocked by *Simkania* infection. Tom40 was used as a marker for mitochondria and Actin as a marker for cytosol. n=3

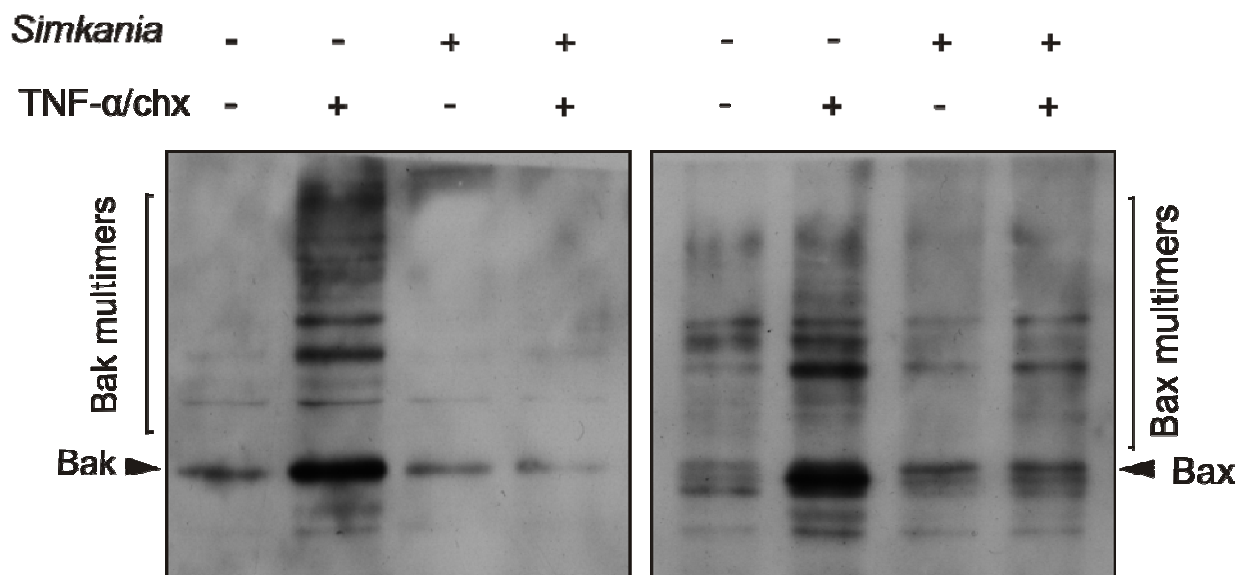


Figure 3.7c. Immunoblot analysis of Bax and Bak after mitochondrial isolation and *in vitro* cross linking. HeLa cells with or without *Simkania* infection (MOI 1, 3 days) were treated with 20 ng/ml TNF- α /3 μ g/ml chx or carrier for 4 h before mitochondria isolation, *in vitro* crosslinking and analysis. Bax and

Bak (black arrows) are not activated in *Simkania*-infected induced cells as shown by background Bax and Bak oligomerisation (brackets). Equal loading was verified by Bradford assay and Tom 40 western blot. Input Bak, Bax and Actin showed no differences in expression or loading. n = 2.

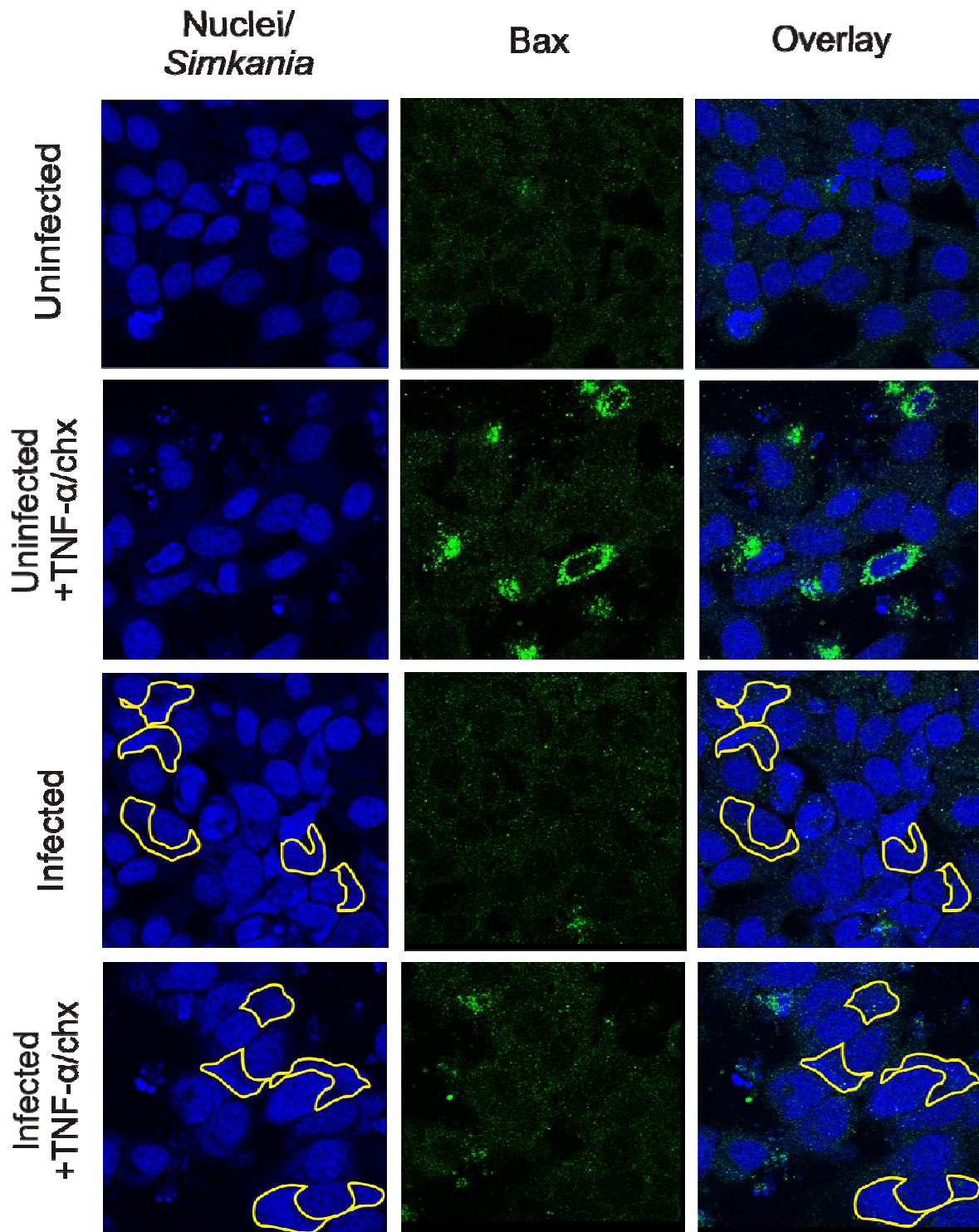


Figure 3.7d. Immuno fluorescence staining of active Bax with a conformation sensitive antibody after *Simkania* infection. HeLa cells were treated as described in Figure 3.7a. Images show mitochondrial localization of active Bax (green) in control-induced cells. Bax was not activated in TNF- α /chx treated *Simkania*-infected cells, n=3.

3.8. Pro-apoptotic BH3-only proteins are not degraded in *Simkania* infected cell

Inhibition of apoptotic signaling upstream of mitochondria has previously been shown to involve Bcl-2 family members in *Chlamydia*-infected cells (Fischer et al, 2004b). One mechanism involves the degradation of pro-apoptotic BH3-only proteins acting to either directly or indirectly induce Bak and/or Bax oligomerisation and mitochondrial outer membrane permeabilization (Dong et al, 2005; Ying et al, 2005).

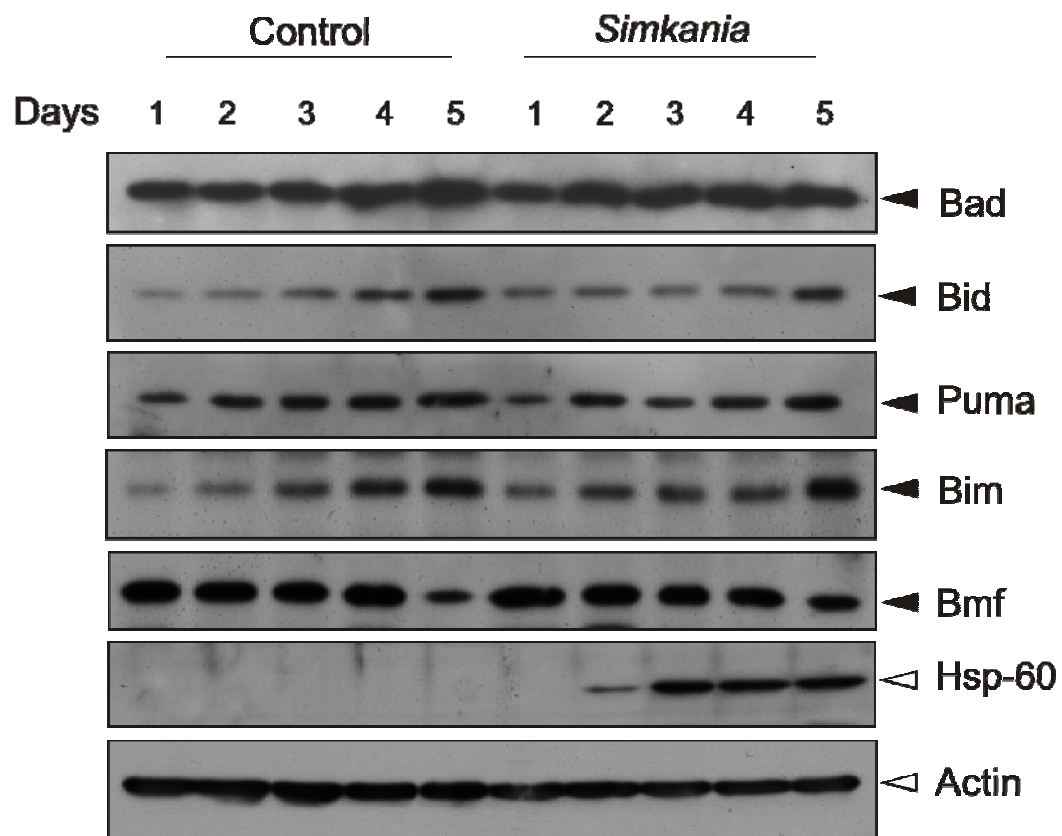


Figure 3.8. Immunoblot analysis of the pro-apoptotic BH3-only Bcl-2 family members during *Simkania* infection. HeLa cells were infected with *Simkania* or Mock (control) (MOI 1) in a time course experiment before analysis. The BH3-only proteins (Bad, Bid, Puma, Bim, Bmf, black arrowheads) are not degraded in *Simkania*-infected cells. Hsp 60 and Actin (white arrowheads) were used as loading controls. n = 2

Hence it was tested whether this is similar in *Simkania* infection. HeLa 229 cells were infected with Sn for different time points from day 1 to day 5, the cell lysates were blotted against Bad, Bid, Bim, Puma and Bmf antibody. No degradation of the BH3-only proteins was detectable (Figure 3.8). This proves that the resistance to apoptosis in Sn-infected cells does not depend on the regulation of the pro apoptotic BH3-only proteins.

3.9. Anti-apoptotic Bcl-2 family members are not regulated in Sn-infected cells

The regulation of anti-apoptotic Bcl-2 family members Bcl-2 and Mcl-1 were also tested during the time course of Sn infection. Mcl-1 has previously been found to be up regulated and stabilized in *C. trachomatis* infection, Mcl-1 was also critical for apoptosis resistance in Ctr-infected cells (Bohme et al; Rajalingam et al, 2008b; Sharma & Rudel, 2009).

Interestingly, Mcl-1 and Bcl-2 levels remained constant in a time course infection experiment (Fig. 3.9), indicating that regulation of the Bcl-2 family members does not account for the apoptosis resistance in *Simkania* infection.

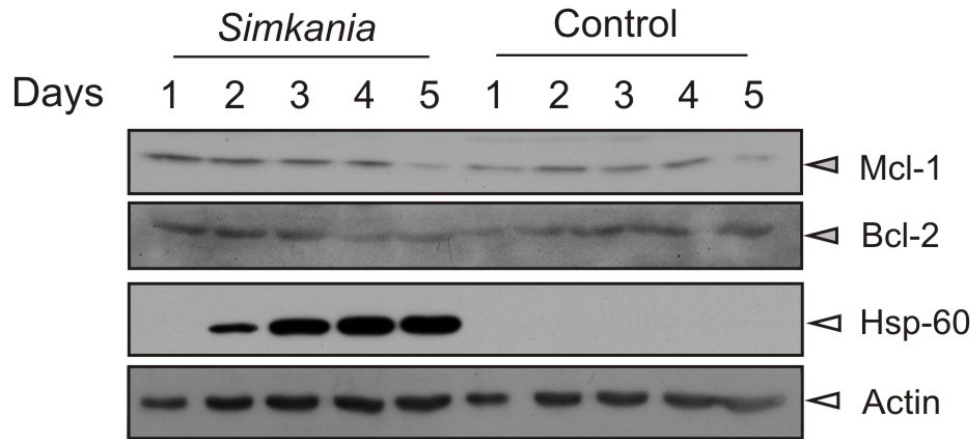


Figure 3.9. Immunoblot analysis of the anti-apoptotic/pro-survival signaling during *Simkania* infection. HeLa cells were infected with *Simkania* or Mock (control) in a time course experiment before analysis. Anti-apoptotic Bcl-2 family members like Mcl-1 or Bcl-2 (grey arrowheads) are not regulated. Akt is strongly activated during infection (black arrowheads). Hsp 60 and Actin (white arrowheads) were used as loading controls. n = 2.

3.10. NF- κ B is activated upon Sn infection

NF- κ B comprises a family of highly regulated dimeric transcription factors that play a pivotal role in inflammatory responses and immunological reactions and are required for apoptosis resistance in *C. pneumoniae* infection (Paland *et al.*, 2006). To test the relevance of NF- κ B signaling in *Simkania* infection, the degradation of I κ B- α after *Simkania* infection was tested. The HeLa cells infected with Sn for 72 h were induced with TNF- α in the absence of chx for time points, ranging from 5 min to 60 min. The cells lysates were blotted and probed against I κ B antibody, to find that I κ B was degraded in induced cells. Surprisingly the uninduced Sn-infected (72 h) cells also lacked the expression of I κ B, which is the clear indication that NF- κ B is activated upon Sn infection (Figure 3.10a).

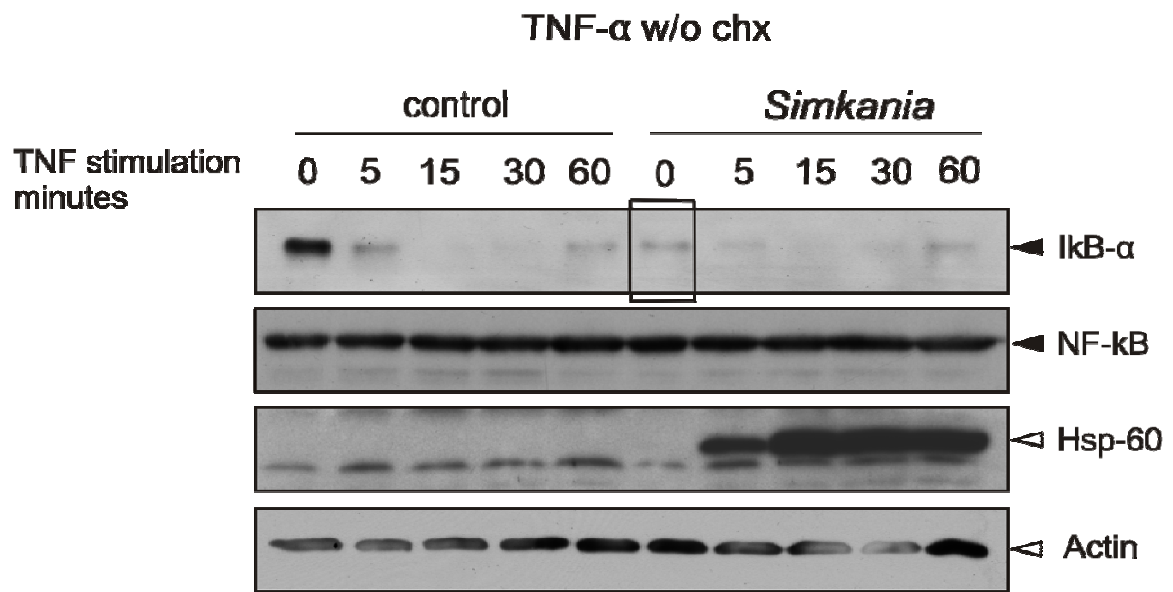


Figure 3.10a. HeLa cells with or without *Simkania* infection (MOI 1) were treated with 20 ng/ml TNF- α without chx for 5, 15, 30 and 60 min to activate the MEK-ERK pathway. The regulation of I κ B is presented above. The figure shows that even without any TNF- α activation after 3 dpi I κ B is ubiquitinated and degraded (black arrowheads) and the total p65 remains unaffected, indicating that the NF- κ B is activated upon infection. Actin is used as the loading control, n = 2.

Infected cells were nearly completely depleted of I κ B- α similarly as non-infected control cells upon TNF- α stimulation without chx. Hence to further investigate and confirm, Sn-infected cells (72 hpi) were stained for p65 (RelA) an important subunit of NF- κ B, which gets transported to the nucleus upon NF- κ B activation. Figure 3.10b shows that NF- κ B gets clearly activated upon Sn infection.

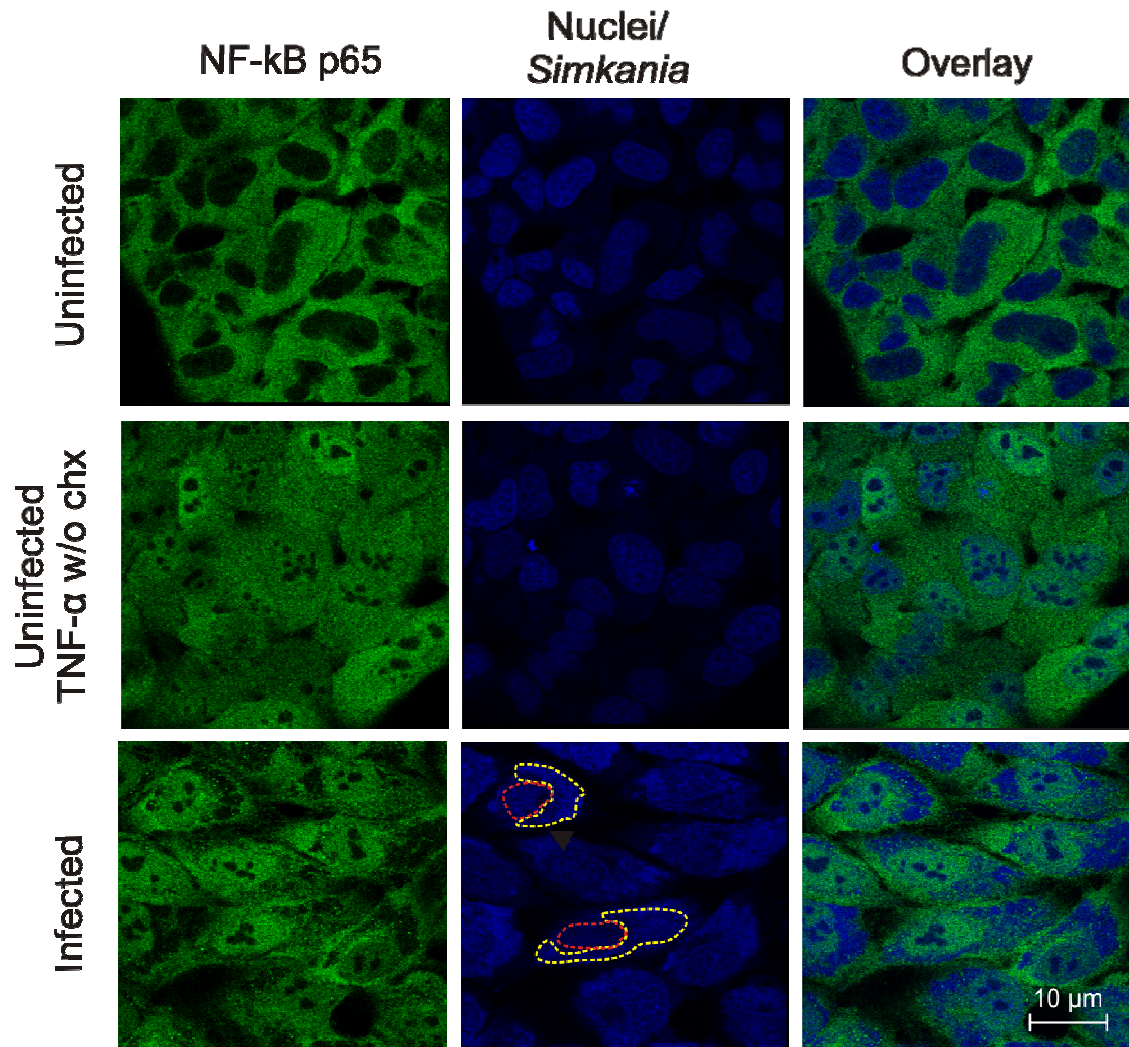


Figure3.10b. Immunofluorescence staining of p65 component of NF- κ B in uninfected, uninfected TNF- α treated and 3 days Sn infected cells. P65 (green) is detected to be in the nucleus in the TNF- α treated control cells as expected, while the same is also detected in Sn infected cells. P65 is hardly activated in the control cells. The nucleus is labeled with Draq5 (blue), which intercalates in the DNA of the cell as well as the bacteria, n=2.

Consistent with the activation, NF- κ B is translocated to the nucleus in infected cells similar as upon TNF- α stimulation. To investigate the binding of NF- κ B subunits to the nuclear DNA, Electro Mobility Shift Assay (EMSA) was performed (in collaboration with Dr. Bhupesh Prusty) as described in the Method (2.2.14). The

Figure 3.10c shows the EMSA result, which indicates that NF- κ B gets activated, revealing increased binding of NF- κ B to an oligonucleotide comprising an NF- κ B consensus motif upon 48 hpi with Sn and it is the maximum at 72 hpi at which they resist apoptosis. At the later time point of 4 dpi, the activation clearly goes down.

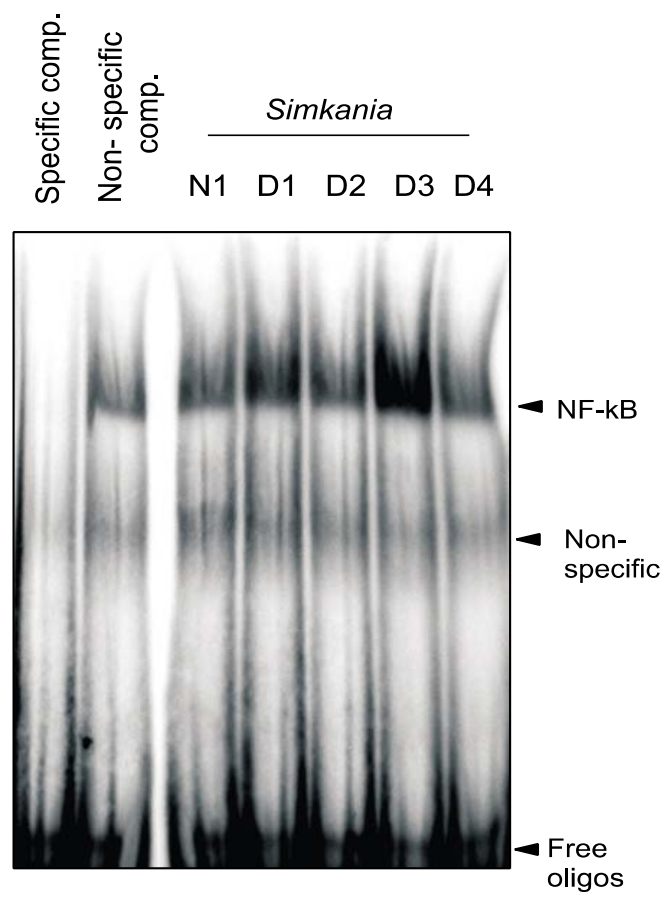


Figure 3. 10c. To confirm if NF- κ B binds to the nucleus in infected cells, the HeLa 229 cells were infected with Sn from day 1 to day 5 and the cells were taken up for EMSA (in collaboration with Dr. Bhupesh K Prusty). The nuclear extract was made and incubated against radioactive labeled probes. The samples were run on 6 % PAGE and developed. EMSA clearly shows that NF- κ B is activated upon infection with Sn, n=2

3.11. NF- κ B activation is necessary for apoptosis resistance

The next question that rose was if NF- κ B activation was required for the apoptosis resistance in Sn-infected cells. HeLa 229 cells were plated and treated with NF- κ B specific inhibitor CAPE, a cell permeable active component of propolis from honeybee hives.

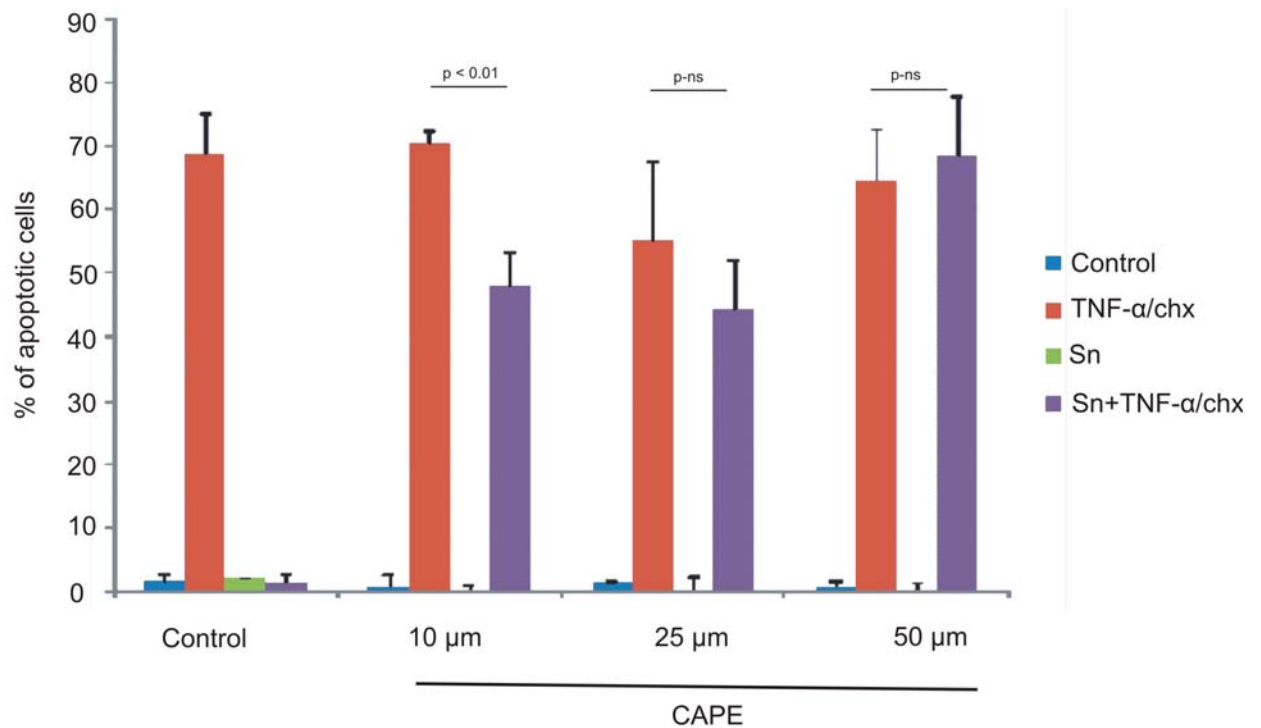


Figure 3.11a. Bar diagram showing the percentage of apoptotic cells. Sn infected HeLa 229 cells were treated with CAPE (NF- κ B Inhibitor) on 3 dpi for 5h and induced with 20 ng/ml TNF- α /3 mg/ml chx or carrier for 4 h before analysis. The cells were fixed and stained for Hoechst, the apoptotic and healthy cells were counted under 40x magnification, five fields per sample, n = 2, Error bars = SE n = 2.

The HeLa 229 cells were plated and treated with 25 μ M of CAPE for 5 h after 3 dpi with Sn infection and were induced for apoptosis using TNF- α and chx as described in Methods. After 4 h of induction the cells were harvested for immunoblotting for PARP cleavage (as shown in figure 3.11b). A similar experiment

was performed for immunofluorescence to access the percentage of apoptosis (Figure 3.11a). CAPE treatment led to decrease in apoptosis resistance and the infected cells were more sensitized to apoptosis than the untreated cells.

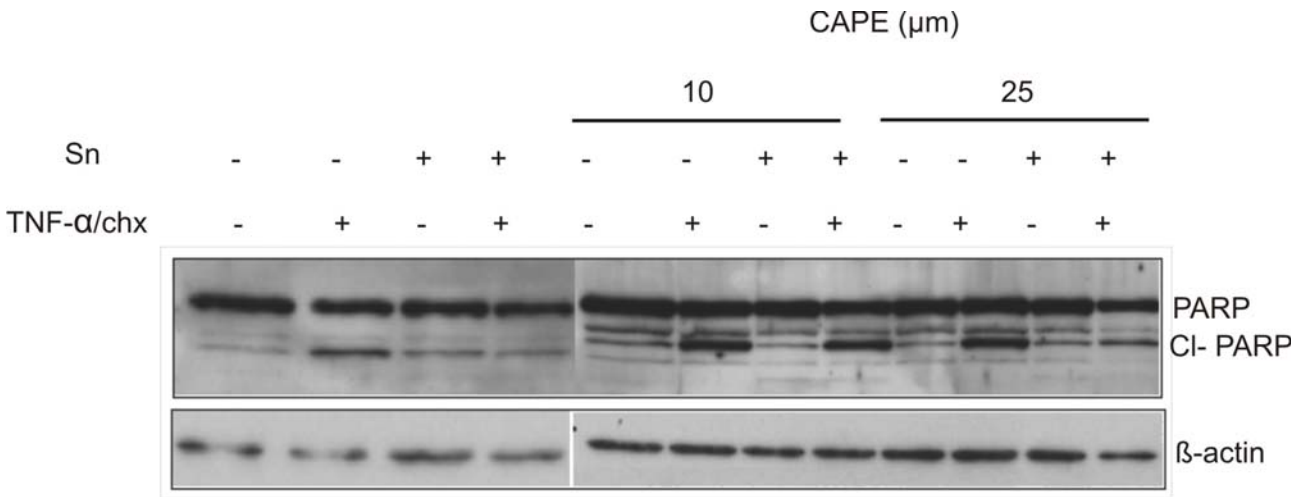


Figure 3.11b. Immunoblot analysis of PARP cleavage in *Simkania* infected cells after treatment with NF-κB inhibitor. *Simkania*-infected HeLa 229 cells were treated with CAPE (NF-κB Inhibitor) on 3 dpi for 5 h and induced with 20 ng/ml TNF-α/3 μg/ml chx or carrier for 4 h before analysis. PARP cleavage was a measure of apoptosis sensitization. Treatment with 10 μM CAPE clearly sensitized infected cells to apoptosis. Hsp60 and Actin were used as loading controls.n = 2.

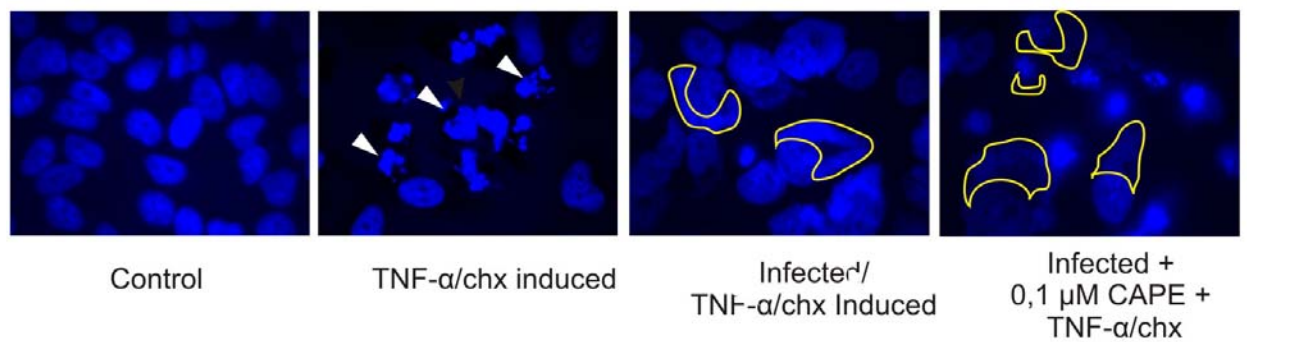


Figure 3.11c. Immunofluorescence of samples treated as described in Figure 3.11b. Samples were stained with Hoechst (blue) and viewed under a fluorescence microscope for counting. Hoechst dye stained both HeLa cell nuclei and *Simkania* inclusions. White arrowheads mark example apoptotic cells, n = 2.

3.12. NF- κ B mutation affects the infectivity of Sn

As NF- κ B was strongly activated during infection it was interesting to check whether NF- κ B activation is required for the development of bacterial inclusion and infectivity.

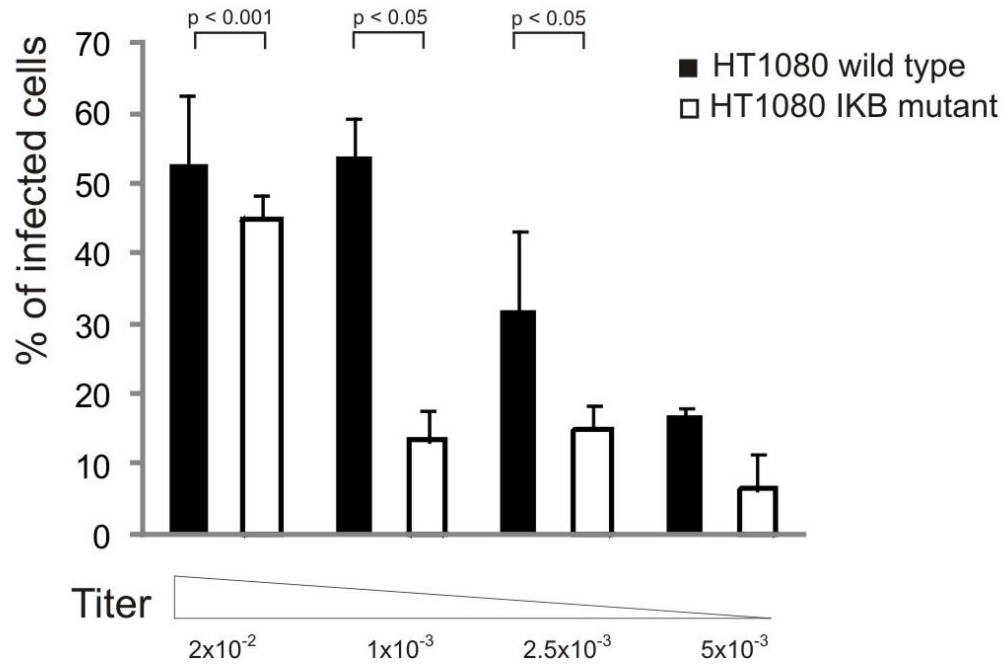


Figure 3.12a. Bar diagram showing the *Simkania* infectivity assay. HT1080 wild type (fibrosarcoma cells) and I κ B mutant cells were infected with *Simkania* at a MOI 1 for 3 days titrated on fresh HeLa monolayers and stained. *Simkania* positive cells were counted to determine differences in primary infection between the two cell lines (40x magnification, five fields per sample, n=2, Error bars = SE). Bacterial growth was strongly reduced in I κ B mutant cells.

Since the developmental cycle of Sn takes 3-5 days, inhibitor treatment was not feasible for this experiment due to toxicity upon long-term treatments. Therefore HT1080 cell line, which expresses a non-degradable I κ B derivative, which sequesters NF- κ B p65 in the cytosol, was used (Wang *et al.*, 1996).

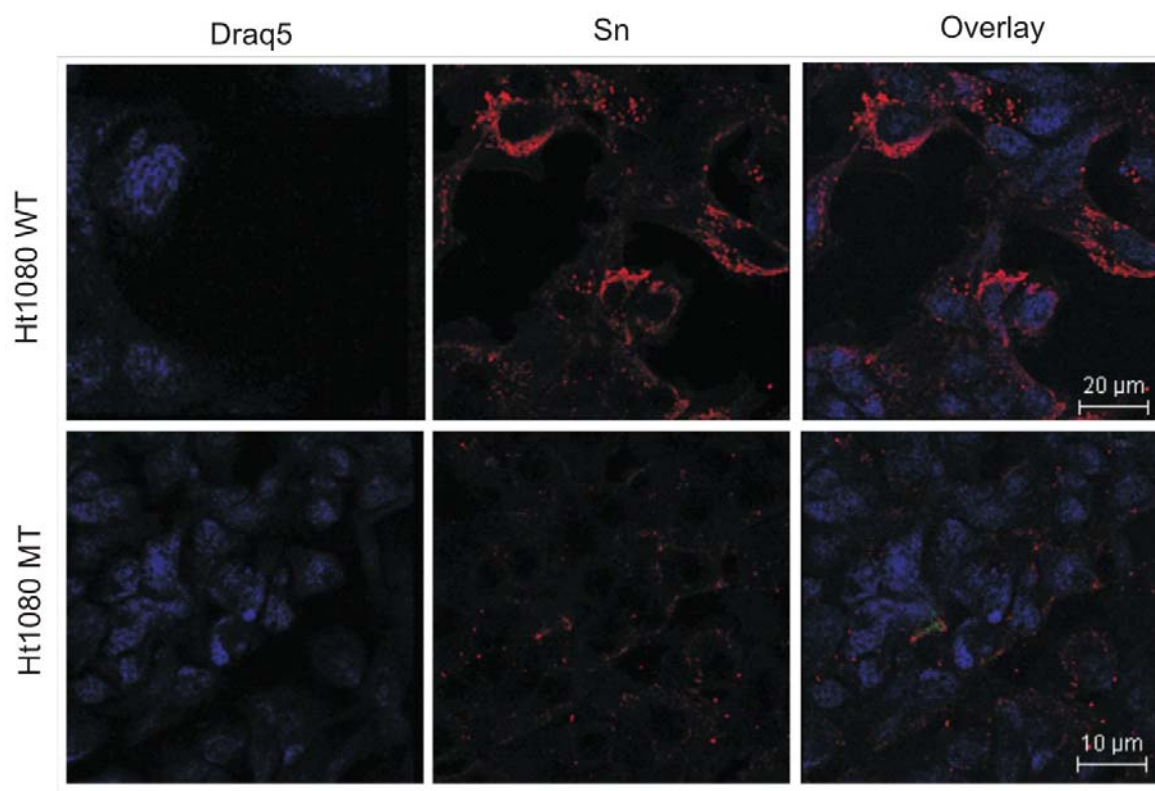


Figure 3.12b. Immunofluorescence analysis of HT1080 wt and IkB mutant cells infected with Sn. the cells are stained with Draq5 (blue) and with Sn antibody (red). The HT1080 WT cells are stained more with Sn than the IkB mutant cells showing that the mutants have defect in promoting Sn infection, $n=3$

The cells were infected with Sn and taken up for infectivity assay. After 72 hpi, the infected cells were lysed using glass beads or freeze thawing at -80°C . The lysate was used to infect freshly plated HeLa cells in different dilutions. After second round of infection for 72 h the cells were fixed with 4% PFA and stained with Hoechst and taken up for microscopy. The percentage of infected cells were calculated and used for making the graph as represented in Figure 3.12a. Surprisingly, the expression of non-degradable IkB resulted in decreased infection and infectivity in Sn (Fig. 3.12a), suggesting a role of NF- κB transcribed genes in the replication of Sn.

3.13. Akt is activated in *Simkania* infected cell

To further determine the origin of *Simkania*-mediated anti-apoptosis the major survival pathway directly involved in TNFR signaling, PI3 kinase pathway was analysed. It has been reported that Akt/protein kinase B inhibits apoptosis by preventing the release of cytochrome c from mitochondria (Brazil et al, 2002; Kennedy et al, 1999). Since PI3 kinase pathway is a major survival pathway, Sn infected cells after different time points were probed against Akt and pAkt antibody, revealed that Akt was indeed strongly phosphorylated in infected cells (Figure 3.13). The phosphorylation was very prominent after 3 dpi and gradually reduced after day 4. This data very much supports the resistance that this bacterium promotes on apoptosis induction.

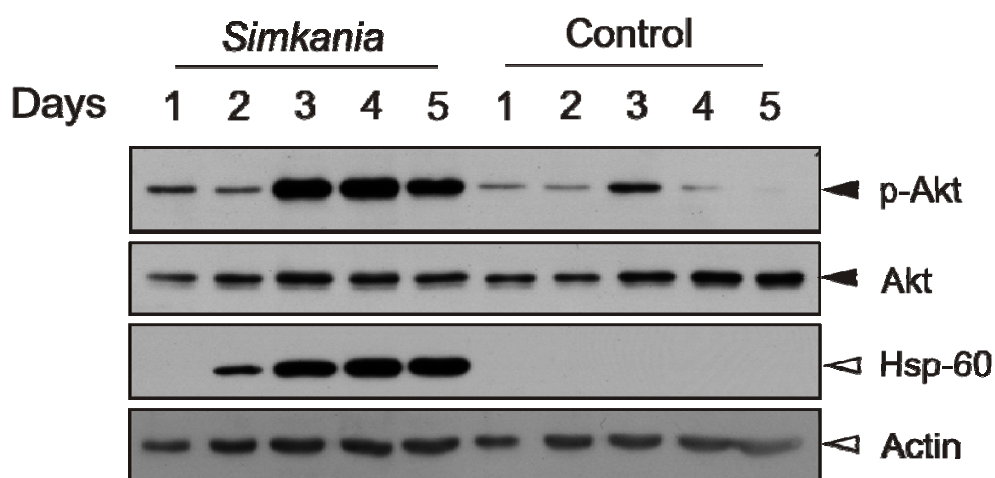


Figure 3.13. Immunoblot analysis of the anti-apoptotic/ pro-survival signaling during *Simkania* infection. HeLa cells were infected with *Simkania* or Mock (control) in a time course experiment before analysis. Anti-apoptotic Bcl-2 family members like Mcl-1 or Bcl-2 (grey arrowheads) are not regulated. Akt is strongly activated during infection (black arrowheads). Hsp 60 and Actin (white arrowheads) were used as loading controls, n = 2.

3.14. Activation of PI3 kinase pathway is required for apoptosis inhibition in Sninfected cells

As PI3 kinase is a major survival signal, it was important to find if its activation is necessary for the resistance to apoptosis. To test whether activation of Akt is required for apoptosis inhibition, inhibitor experiments were performed. The Akt pathway was investigated by blocking the upstream activator phosphatidylinositol 3-kinase (PI3K) using LY-294002 (Vlahos et al, 1994). The inhibitor is cell permeable and binds directly to the ATP binding site of the enzyme.

Treatment of infected HeLa cells (3 dpi, MOI 1) with LY-294002 (dilution described in 2.2.9) for 2 h before induction of apoptosis resulted in a marked dose-dependent apoptosis sensitization (Figure 3.14a) as judged from PARP cleavage and apoptotic cell count. Different dilutions of the inhibitor were tested to find that the effect is gradual and not an artifact. These results show that the activity of Akt is required in *Simkania*-infected cells to resist apoptosis induction. Different dilutions ranging from 0.1, 1.0 and 10 μ M were tested and the percentage of apoptotic cells rose gradually from 14.7 % to 46% and 66% respectively. This data clearly state that PI3 kinase signaling pathway is necessary to block resistance in Sn-infected cells.

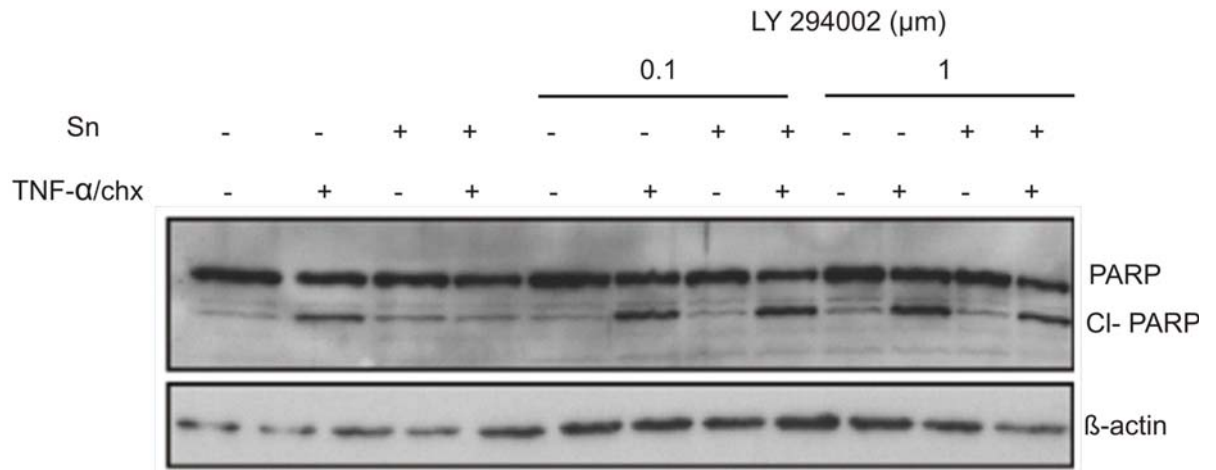


Figure 3.14a. Immunoblot analysis of PARP cleavage in *Simkania*-infected cells after treatment with PI3K inhibitor. *Simkania*-infected HeLa 229 cells were treated with Ly294002 (PI3 kinase Inhibitor) on 3 dpi for 2 h and induced with 20 ng/ml TNF- α /3 $\mu\text{g/ml}$ chx or carrier for 4 h before analysis. PARP cleavage was a measure of apoptosis sensitization. Treatment with 0.1 mM LY29004 clearly sensitized infected cells to apoptosis. Hsp 60 and Actin were used as loading controls, $n = 2$.

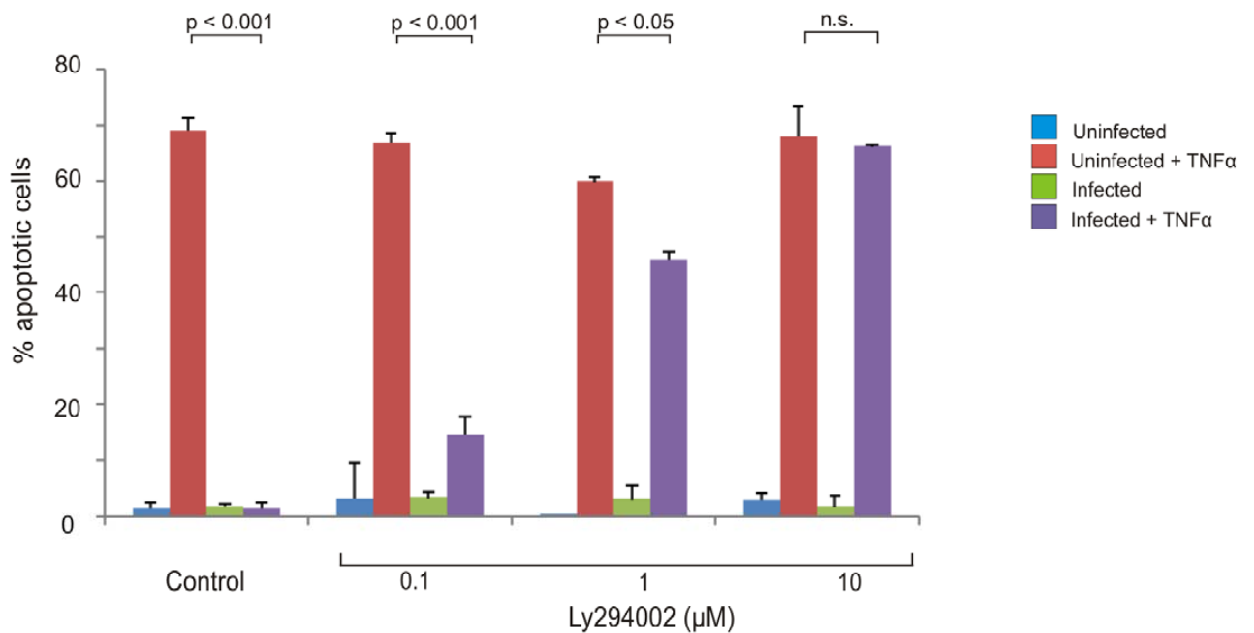


Figure 3.14b. Bar diagram showing samples treated similar as in Figure 3.14a but prepared for immunofluorescence analysis. Hoechst stained cells were counted to determine the number of

apoptotic cells (40x magnification, five fields per sample, n = 2, Error bars = SE). 1 mM LY29004 was found to restore apoptosis sensitivity to 70% of control.

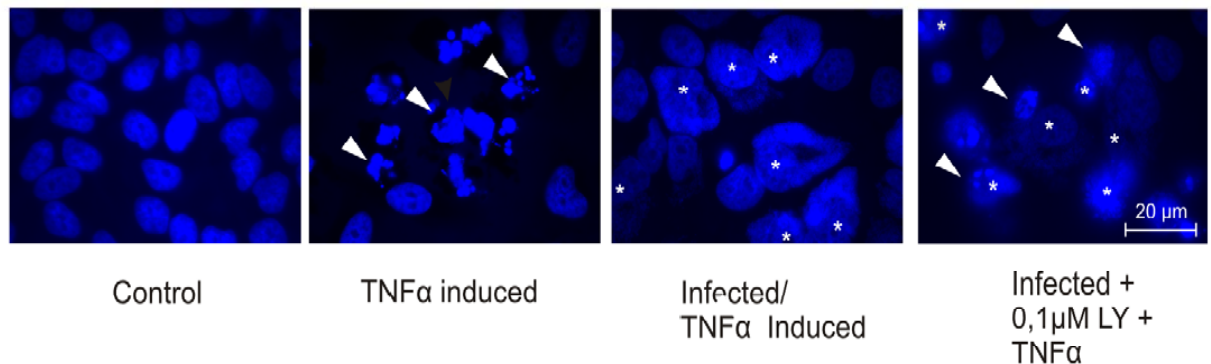


Figure 3.14c. Immunofluorescence of samples treated as described in Figure 3.14b. Samples were stained with Hoechst (blue) and viewed under a epifluorescence microscope for counting. Hoechst dye stained both HeLa cell nuclei and *Simkania* inclusions. White arrowheads mark example apoptotic cells. White asticks mark the infected cells. n = 2.

3.15. cIAPs are up-regulated and required for apoptosis resistance in Sn-infected cells

It is already reported that Inhibitor of apoptosis proteins (IAPs) plays a vital role in apoptosis inhibition of *C. pneumoniae* and *C. trachomatis*-infected cells (Paland et al, 2006a; Rajalingam et al, 2006b). Hence, the regulation of IAPs in Sn infected cells was under investigation. Interestingly in a time course western blot of the infected sample we found that cIAP-1 and cIAP-2 were up regulated in the course of infection (Figure 3.15a).

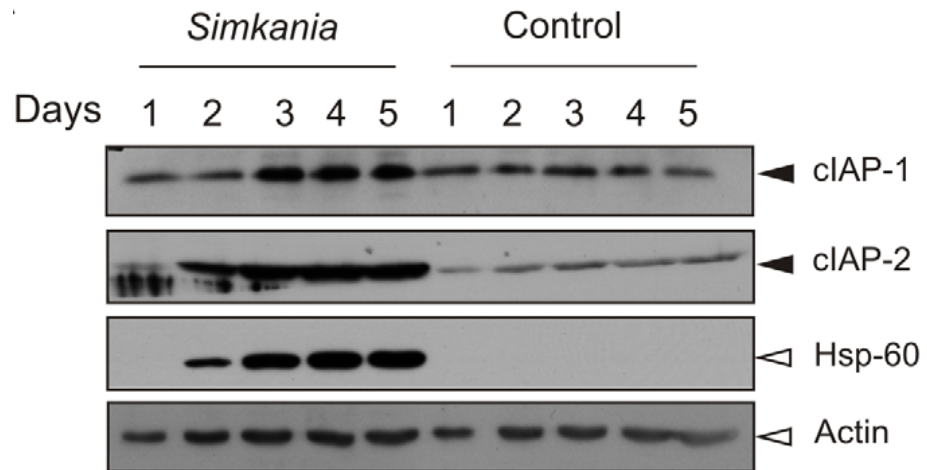


Figure.3.15a. Immunoblot analysis of the anti-apoptotic/pro-survival apoptosis regulators during *Simkania* infection. HeLa cells were infected with *Simkania* or Mock (control) (MOI 1) in a time-course experiment before analysis. Anti-apoptotic cIAP-1 and -2 (black arrowheads) are strongly upregulated. Hsp-60 and Actin (white arrowheads) were used as loading controls, n = 2.

The up-regulation or stabilization was well pronounced after 48 hpi. Since the antibody against XIAP did not work, RT PCR was done to analyze the levels of XIAP mRNA over a time frame of infection. HeLa cells were infected with Sn for a time frame of day1 to day 5 and the RNA was isolated as explained above in methods 2.2.15. The RNA was used for real time analysis of expression over time frame. The results show an up regulation of XIAP after 24 hpi. All this data explains how Sn resists apoptosis over a longer time period when compared to other *Chlamydiales*.

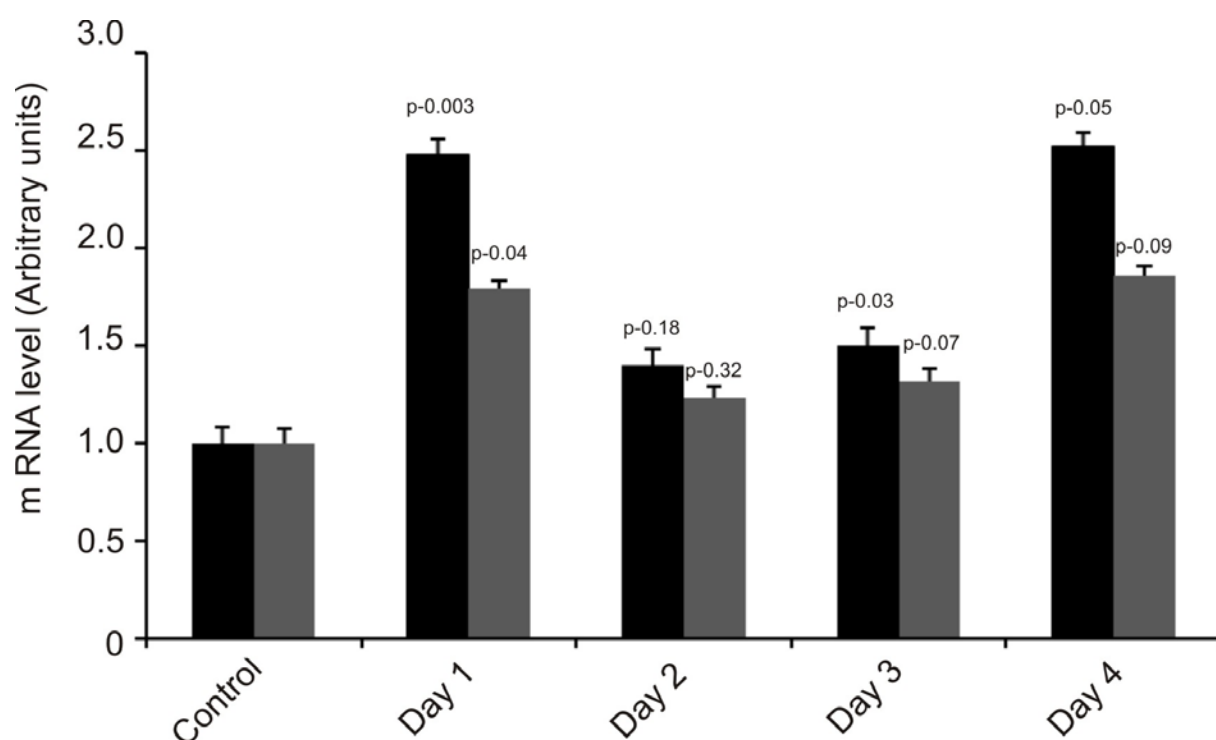


Figure 3.15b. HeLa 229 cells were infected with Sn for different days (1-5). The RNA from the cells was isolated as explained in methods. The RNA was converted into cDNA and taken for qRT-PCR to detect the relative amount of the targeted genes. Upon Sn infection the gene expression of cIAP-1 (black) as well as XIAP (grey) was increased. The experiment was repeated three times to calculate the standard deviation.

To prove, if these IAPs are required to maintain the high apoptosis resistance in infected cells. Expression of cIAP-1 and cIAP-2 was silenced in control and infected cells using specific siRNAs and induced with TNF- α /chx for apoptosis.

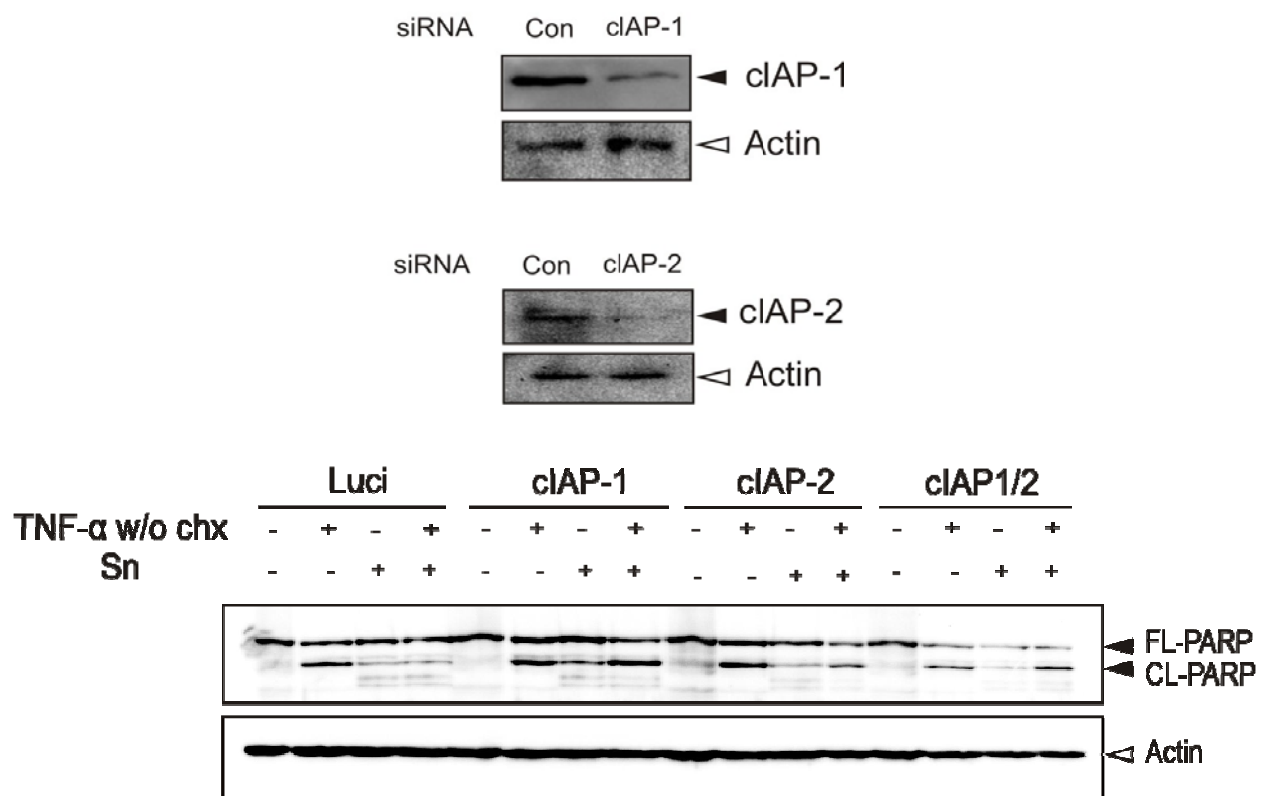


Figure.3.15c. Immunoblot confirmation of cIAP-1 and -2 knock down. HeLa cells were transfected with siRNA directed against cIAP-1, -2 or Luciferase (control). cIAP-1 and -2 (black arrowheads) were strongly down regulated at day 3 post transfection. Actin (white arrowheads) was used as loading control. n = 2. Immunoblot analysis of PARP cleavage in *Simkania* infected cells after cIAP-1 and -2 single or cIAP-1/-2 double knockdowns. HeLa 229 cells were transfected for 3 days before *Simkania* infection. On day 3 pi cells were induced with 20 ng/ml TNF- α /3 μ g/ml chx or carrier for 4 h before analysis. PARP cleavage (black arrowheads) was a measure of apoptosis sensitization. Single knockdown of either cIAP-1 or -2 or both clearly sensitized infected cells to apoptosis. Actin (white arrowhead) was used as loading control. n = 2.

The infected cells were found to be sensitized for apoptosis in the absence of cIAP-1 and cIAP-2 (Figure 3.15c), supporting their role in blocking apoptosis in infected cells. The percentage of apoptotic cells upon TNF- α /chx induction rose from

14 % in untreated infected cells to 48% in cIAP-1 knock down cells, while in the case of cIAP-2 knock down cells, the percentage of apoptotic cells still raised higher to about 54%. This clearly depicts the importance of IAPs in apoptosis resistance in Sn infected cells.

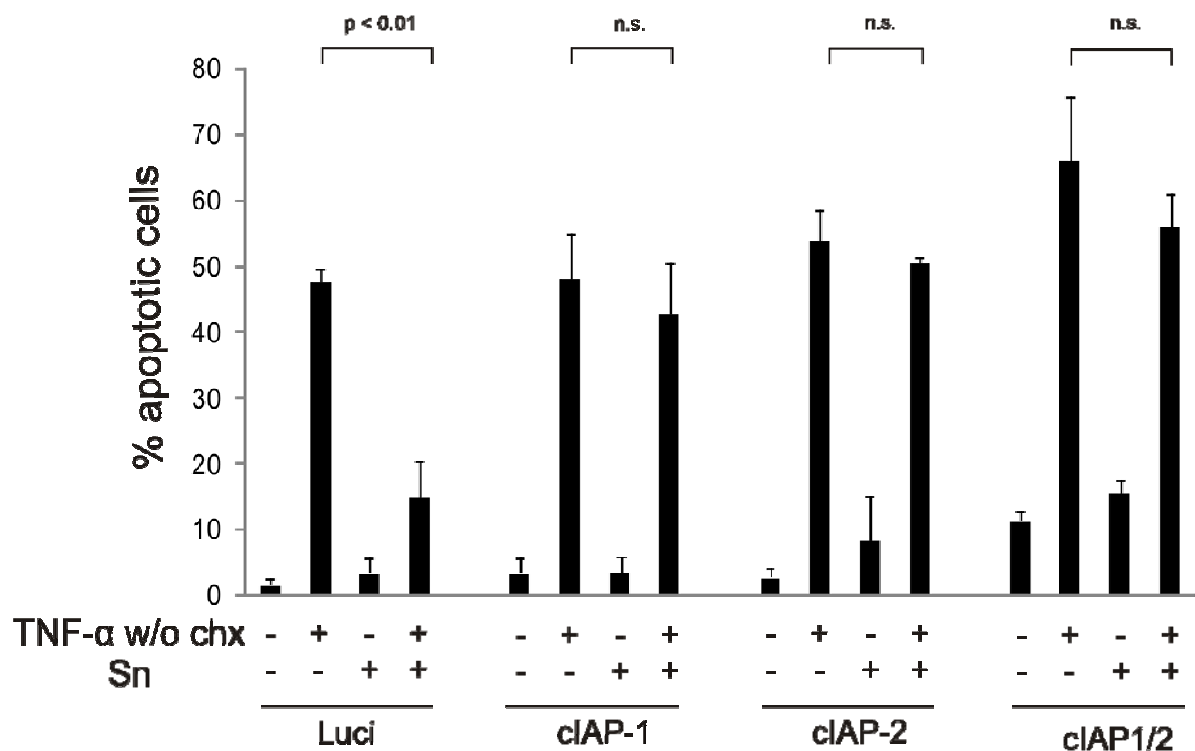


Figure 3.15d. Bar diagram showing samples treated similar as in Figure 3.15c but prepared for immunofluorescence analysis. Hoechst stained cells were counted to determine the number of apoptotic cells (40X magnification, five fields per sample, n = 2, Error bars = SE). Single knockdown of either cIAP-1 or -2 or both was found to restore apoptosis sensitivity to 70% of control.

3.16. Sn protects *Acanthamoeba castellanii* during starvation

As *A. castellanii* is one of the natural hosts of Sn, it was interesting to investigate the amoeba-Sn interaction. *A. castellanii* cells were plated in 12-well plate, after 24 h the amoeba converted from the dormant cyst form to the proliferative

trophozoite form and settled down at the bottom of the plate. The cells were infected with different MOI of Sn ranging from 10 to 100.

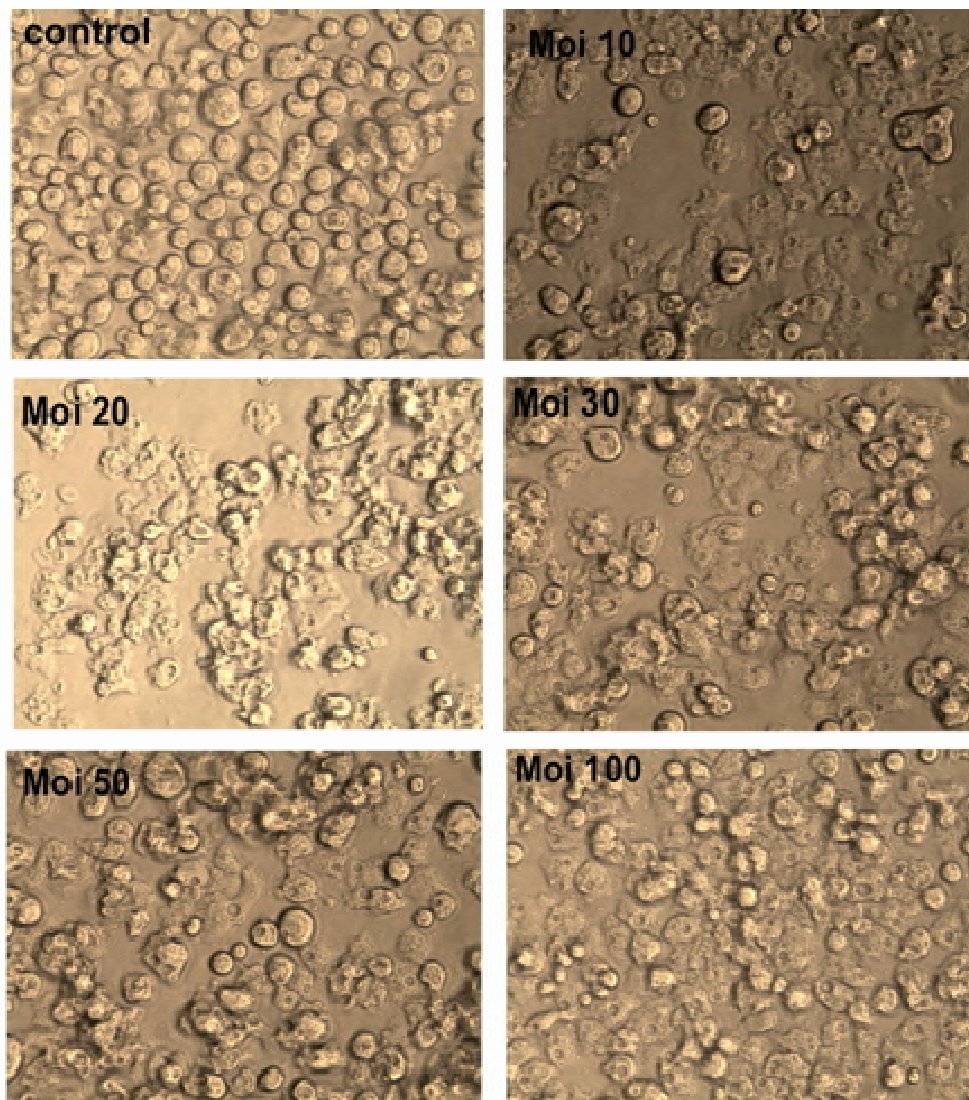


Figure 3.16. *Acanthamoeba Castellanii* cells were seeded in 12 well plate and after 24 hpi with different MOI of Sn, the cells were starved for 16h. The uninfected control cells converted into the inactive and harsh environment tolerating csyts form while the Sn infected cells, in a MOI dependent manner continued to survive in the trophozoite form. n=3

After 24 hpi the cells were washed with phosphate buffer saline and incubated in the encystment media for starvation. It was interesting to observe that after 16 h, the starved uninfected cells converted from the trophozoite form to the cyst form

indicating the unfavorable condition for survival. Surprisingly as Figure 3.16 indicates the Sn infected cells could survive in the starving environment and continued in the proliferative and nourishing trophozoite form. The higher the MOI of Sn infection the better was the survival in the trophozoite form, indicating that Sn protects the amoeba to overcome unfavorable environment.

4. Discussion

4.1. Resistance to apoptosis is highly conserved in the order *Chlamydiales*.

Apoptosis resistance has been a common denominator as an outcome of infection and likely prerequisite for the development of obligate intracellular pathogenic *Chlamydia*. Here, in this study it is demonstrated that like other *Chlamydiales*, the evolutionary related bacterium *Simkania negevensis* is also able to block host cell apoptosis. Sn infection could block the apoptotic pathway at multiple levels by modulation of specific host cell factors. It is evident from the results described above that anti-apoptotic and survival mechanisms are widely conserved in the order *Chlamydiales*. Although the mechanisms involved is not completely revealed, the ability to replicate and maintain long-term relation in the host cell seems to significantly contribute to chlamydial pathogenicity. These intracellular parasites maintain a delicate balance between exploiting and protecting their host by hijacking the signaling pathways in the host cell. Interestingly these pathogens selectively, either up-regulate or stabilize the anti-apoptotic proteins and down-regulate or degrade the pro-apoptotic proteins by means of their proteases. Although *Chlamydiales* are known to resist apoptosis in the productive growth as a path of survival they are also known to inhibit apoptosis during persistent growth or in phagocytes but induce apoptosis in T cells, which indicates that modulating apoptotic pathways have an immunomodulatory role in chlamydial infections (Miyairi & Byrne, 2006). An exception to this rule may be *Parachlamydia*, which appears to survive in human macrophages, but eventually triggers apoptosis (Greub et al, 2003). The inability to induce apoptosis inhibition may be one reason why *Parachlamydia* does

not replicate in most mammalian cell types (Matsuo et al, 2008). Interestingly Gimenez et al (2011) have reported about cross-talk between intra-amoeba pathogens. They could identify potential horizontal gene transfers between *Legionella* and *Chlamydiales*. But, it is still unclear whether *Simkania* and *Parachlamydia* are able to influence death of amoebae. The type 1 metacaspase in amoeba is known to regulate temperature fluctuations. At a lower temperature, metacaspase is over expressed and this induces the encystation of *Acanthamoeba castellanii*. This is associated with a reduced number of bacteria within amoeba (Ohno et al, 2008). Although, metacaspases are already known for their role in PCD (Suarez et al, 2004) their natural substrate remained unknown until Sundstrom et al (2009), reported that tudor staphylococcal nuclease (TSN) is cleaved by metacaspases. The human TSN is a substrate of caspase-3 during apoptosis; this impairs its ability to activate mRNA splicing and inhibits its ribonuclease activity. Sn infection could maintain the trophozoite form of the amoeba under starvation, which indicates that Sn could regulate some genes in amoeba for its survival and thus they successfully maintained a symbiotic association. Recently, Song et al (2012) reported that Atg-16 mediated autophagy is required for the encystment of *Acanthamoeba castellanii*. From this data one tempts to assume that Sn infection might also interfere with autophagy, since it is an innate immune mechanism employed by the host cell to clear infection. Sn infection might prevent autophagy and thus hinder the encystment of amoeba. This indicate that Sn have derived its ability to resist apoptosis as well as to evade autophagy, by co-evolving in amoeba. Signaling to cell death inhibition initially could have co-evolved as a consequence of the *Simkania*-amoebae interaction and could

have later been exploited during the exposure to mammalian cells. Adaptation to different hosts may, at least in part, explain the differences we observed in anti-apoptotic signaling between cells infected with members of *Chlamydiales* adapted to amoebae (*Simkania*) and mammalian cells (*C. trachomatis*, *C.pneumoniae*).

4.2. Sn resists apoptosis in infected cells in a time and MOI-dependent manner

The apoptosis inhibition in *Chlamydiales* depends on its developmental cycle, with the onset early after EB to RB transition and maximum during RB replication (Fan et al, 1998a). The developmental cycle of *Simkania* lasts up to 10 days and therefore significantly longer than that of *C. trachomatis* (48 h) and *C. pneumoniae* (72–96 h) under comparable infection conditions. It was therefore unexpected to see that even at a MOI of 0.5, conditions, where hardly one EB infects one cell; about 50% of the cell were protected from apoptotic stimuli already at 24 hpi and almost all infected cells were completely protected at 3 dpi. A similar efficient protection at such low MOI has neither been observed with *C. trachomatis* (Fan et al, 1998a) nor with *C. pneumonia* (Fischer et al, 2001; Rajalingam et al, 2001b). The infected cell remained resistant for apoptotic stimuli up to 4 dpi indicating that *Simkania* has evolved highly efficient and long-lasting mechanisms to block host cell death, which is evident from the regulation of the survival factors throughout the completion of its life cycle. Similar to *C. trachomatis* infection, cells infected at higher MOI acquired apoptosis resistance earlier (Figure 3.3c.), which has been suggested to be dependent on the rapid entry of the bacteria into the replicative phase of the developmental cycle (Fan et al, 1998a). Interestingly, similar as with *C. trachomatis*, infection with *Simkania* at a higher MOI up to 100 had no visible cytotoxic effect, whereas significant cytotoxicity

already starting at a MOI of 10 has been reported for *C. pneumoniae* infection (Rajalingam et al, 2001b). The infected cells blocks apoptosis even though bacteria were cultured in cycloheximide containing media (an inhibitor of host cell protein biosynthesis). However it was observed that block in upregulation of proteins like IAPs and inhibiting the activation of survival factors like NF- κ B sensitized the infected cells to apoptosis. This indicates that host protein production is also required for imparting resistance. Different to what has been reported for *C. trachomatis* infected McCoy cells, Sn did not induce apoptosis in neighboring uninfected cells during any stage of the infection, excluding paracrine apoptosis induction (Schoier et al, 2001). Rather in Sn infection studies, only the non-infected cells tend to apoptosis upon induction, as the bacteria infects the cells asynchronously.

4.3. Sn infection can resist apoptosis signaling upstream of mitochondria

Despite differences in the kinetics of the onset, efficiency and duration of apoptosis resistance, all the above data demonstrate a block in apoptotic signaling at the extrinsic and intrinsic levels. The mechanism underlying apoptosis resistance in *Simkania*-infected cells may thus be very similar to those in cells infected with *C. trachomatis* and *C. pneumoniae*, in which apoptotic signaling via mitochondria is prevented (Fischer et al, 2004a; Rajalingam et al, 2008a). Sn may preserve the mitochondrial function and prevent mitochondrial cytochrome c release by three potential mechanisms. It can block the upstream steps that can perturb mitochondrial function. The degradation or down regulation of pro-apoptotic BH3-only proteins is one of the sensible ways. Similar to the report on *C. trachomatis*-infected cells (Rajalingam et al, 2008a), this complete and strong block of apoptotic signaling was

maintained in the infected cell despite of unchanged levels of BH3-only proteins. In contrast, others have found that chlamydial protease-like activating factor (CPAF) was responsible for degradation of BH3-only proteins in cells infected with *C. trachomatis*, (Dong et al, 2005; Fischer et al, 2004b) indicating that depletion of BH3-only proteins plays a role in blocking apoptosis upstream of the mitochondria in their infection setting. The second way is to up-regulate the expression of anti- apoptotic BH3-only proteins. The mitochondrial membrane proteins Bcl-2 or Bcl-2 like proteins are anti-apoptotic and are able to prevent cytochrome c release and caspase-3 activation. But it is also reported that overexpression of Bcl-2 does not always protect from apoptosis induced by Fas cross-linking (Chiu et al, 1995; Scaffidi et al, 1998; Strasser et al, 1995). Overexpression of Bcl-x_l protein levels failed to block apoptosis induced by TNF- α (Erhardt & Cooper, 1996). On examining the level of Bcl-2 in Sn infected cells, stabilization or up-regulation could not be observed. Hence it is not likely that host Bcl-2 or Bcl-2 like molecules solely mediates the Sn anti-apoptotic activity. As it was reported that Mcl-1 plays a key role in resisting apoptosis in *Chlamydia* infected cells, it was interesting to check the regulation in Sn infection. Mcl-1 as one of the major inhibitors of Bak and Bax activation was neither upregulated nor stabilized in Sn infected cells. Since, Mcl-1 was not regulated upon infection, activation or oligomerisation of neither Bak nor Bax were found in Sn-infected cell treated with TNF- α /chx and cytochrome c was fully retained in the mitochondria of these cells, which explained an inactive caspase-9 after apoptosis induction. Third possibility of protecting the mitochondrial potential loss is the novel anti-apoptotic factors that could be released by the bacteria into the cytoplasm of the

host cells. As Sn anti-apoptotic activity is found to be MOI and time frame dependent, it becomes clear that Sn translation is important for the process. At a higher MOI the bacteria establish in the host much faster, meanwhile at a MOI of 1, by 72 hpi, the cells harbor visible inclusions hence; the maximum percentage of apoptosis inhibition was observed. Sn could harbor some mammalian anti-apoptotic protein homologues, which could prevent apoptosis as reported in the case of Epstein Barr virus. The BHRF1 in EBV are the homologues of mammalian Bcl-2, and it inhibits apoptosis induced by exogenous stimuli, like DNA damaging agents, the calcium ionophore ionomycin and the immunological apoptosis inducing molecules like TNF- α and Fas (Kelly et al, 2006). Another EBV nuclear antigen EBNA2 interferes with apoptosis induced by some stimuli through intrinsic pathway by sequestering Nur77 to the nucleus and preventing its translocation to the cytoplasm where it can induce cytochrome c release from the mitochondria (Lee et al, 2002). This indicates that the microbial homologues of apoptosis suppressors may be more potent than endogenous proteins. Currently it is not known which among the above-mentioned factors might be responsible for the mitochondrial signaling blockage in Sn-infected cells. Unlike in *C. trachomatis* infection, despite the fact that, the anti-apoptotic BH3-only proteins are not regulated upon Sn infection, Sn can protect the cells from membrane permeabilisation and potential loss. Since Sn infection can prevent the caspase activation downstream of mitochondria, it becomes clear that regulation of signals upstream of mitochondria may not be the only mechanism employed by Sn to achieve the strong inhibition to apoptosis.

4.4. Caspases are differentially regulated upon Sn infection

Caspases are regulated during pathogenesis in different ways. *Legionella pneumophila* activates Caspase-1 via flagellum and type IV secretions in response of host IPAF prevented phagosome maturation and led to clearance of infection (Amer et al, 2006). Regulation at the level of these cysteine proteases is critical for extrinsic as well as intrinsic apoptosis pathway. Caspases exist as zymogens are activated by cleavage, which permits their protease activity and degradation of substrates leading to cell death. Infection with any pathogen is recognized by the cells leads to the inflammatory responses and release of cytokines, which binds to its receptor and initiates the cascade of caspase activation. The resistance to apoptosis in Ctr was also accounted on the receptor shedding from the infected cells by activated metalloproteinase, TACE. But upon Sn infection as TNF- α induction lead to a strong downstream cascade of survival signals like MEK and ERK it was clear that the resistance to cell death is not contributed by TACE or other means that lead to reduced display of receptors on cell surface. Activated caspases lead to cell death thereby reducing the chance of pathogen to complete its life cycle. The baculovirus is known to inhibit all types of caspases by a baculoviral p35 protein, by cleaving the reactive site loop and forming a protease-inhibitor complex. In addition cowpox virus inhibits the active site of caspases by serine protease inhibitors. One of the most efficiently used methods by pathogens is to up regulate the cellular inhibitor of caspases, the IAPs. Upon Sn infection by one day of infection itself an upregulation of various IAPs could explain the reduced activation of caspases upon apoptosis induction. But in Sn-infected cells the caspases were differentially regulated. Upon Sn

infection, caspase-8 was activated but the executioner caspase -3 and -9 was prevented from activation upon induction with TNF- α . With the activation and recruitment of complex 1 (consisting of TNFR, TRADD, RIP1 TRAF2), the executioner, caspase-3 normally gets activated. This activation was blocked upon Sn infection, which indicates either the formation of complex 1 is affected or that some bacterial factors directly influence the caspase maturation downstream. The data presented here and the previously published work demonstrates that IAPs play a major role in maintaining apoptosis resistance in cultured cells infected with *C. trachomatis* and *C. pneumonia* (Rajalingam et al, 2006a). IAPs are important regulators of apoptosis that bind directly to caspase-3 and -9 with their BIR domain and thus block their activation. During Sn infection IAPs gets upregulated as shown in the figures, until the pathogen lyse the cells. Hence this could be a possible mechanism by which caspase activation is inhibited. But recently some reports have raised doubts over the ability of IAPs in directly inhibiting the catalytic activity of caspases (Eckelman & Salvesen, 2006). But, abrogation of IAPs using siRNA sensitizes the Sn infected cells to apoptosis. Hence analyzing the apoptosis pathway in IAP knockdown scenario could reveal the dependence of caspase activation on IAPs. However, recent data obtained in pulmonary infection experiments with *C. pneumoniae* in knockout mice suggest an important function of cIAP-1 in innate immune signaling in macrophages (Prakash et al, 2009). A role of IAPs in innate immune signaling is consistent with recent reports demonstrating a role of both, cIAP-1 and cIAP-2 in innate immune signaling rather than in directly inhibiting caspase activation (Gyrd-Hansen & Meier, 2010). Infection may directly influence IAP stability

as these proteins possess E3 ligase activity and control their own stability and the stability of other IAPs (Vaux & Silke, 2005b). In this context the previous description of IAP-IAP hetero complexes implemented in IAP stabilization in *C. trachomatis*-infected cells may also be relevant for *Simkania* infection (Rajalingam et al, 2006a).

4.5. Caspase-8 is activated upon Sn infection

Unlike other *Chlamdiales*, the caspase-8 was found to be activated even in the Sn infected cells without any apoptosis induction but still prevented cells death. During Sn infection the cells were maintained in RPMI containing 5% FCS and 1µg/ml of cycloheximide. Addition of protein synthesis inhibitor reduces the synthesis of the cellular caspase-8 inhibitor, cFLIP, which leads to the accumulation of complex II to the TNFR and leading to caspase-8 activation. A death ligand association independent, activation of caspase-8 is also reported for the induction of autophagy (Laussmann et al, 2011), efficient ways of the host to eliminate pathogens by fusing with endosomes and lysosomes to finally degrade the sequestered material. However Sn should have strategies to modify this pathway as they survive in the host mysteriously. Meanwhile since autophagy is the major pathway for the turnover of cytoplasmic components like mitochondria, peroxisomes, smooth and rough membranes, proteins, lipids, RNA and lysosomes, Sn could also easily modulate autophagy to gain access to nutrients by autophagosomes into the inclusion.

4.6. Akt is activated upon Sn infection

As previously described for *C. trachomatis* (Verbeke et al, 2006) and *C. pneumoniae* (Coombes & Mahony, 2002) infection, *Simkania* infection strongly

activates the PI3K-Akt pathway. Activated Akt promotes cell survival through crosstalk with other signaling cascades like the NF- κ B pathway (Romashkova & Makarov, 1999). Akt has in addition a role in cell survival by increasing the uptake of nutrients, positive regulation of metabolic pathways and maintenance of mitochondrial membrane potential (Plas & Thompson, 2005). There is also a direct link between Akt and cell survival by phosphorylating and inhibiting the function of pro-apoptotic Bad (Datta et al, 2000). Any change in the Akt-specific phosphorylation of sites S116 and S136 in Bad in the course of *Simkania* infection was not observed (data not shown), as has previously been described for *C. trachomatis* infection (Verbeke et al, 2006). The observation that PI3K inhibitors sensitize cells infected with *C. trachomatis* (Rajalingam et al, 2008a) or *Simkania* to apoptosis speaks in favor for an evolutionary conserved role of this central survival pathway in controlling host cell survival during development and replication of *Chlamydiales* in their mammalian hosts. Activation of Akt can favor high expression of cIAP-1 (Gagnon et al, 2003), consistent with elevated levels of IAPs and increased phosphorylation of Akt during the course of infection until day 5. But it is still unknown about the mechanism that leads to persistent activation of Akt. An obvious reason could be that Sn secretes anti-apoptotic factors through their type III secretion apparatus as reported with other pathogens (Francois et al, 2000; Galan & Collmer, 1999; Navarro et al, 2005; Yuk et al, 2000). *Salmonella enterica* secretes effector protein SopB to induce sustained activation of Akt (Knodler et al, 2005b). Concurrently host cell stress could also result in Akt activation. Signaling through Akt is known to play (Dimmeler et al, 1998) a key role in protecting cells from variety of toxic stresses (Cross et al, 1995; Dent et al,

2003). Obligate intracellular pathogens like *Chlamydia* is known to increase mitochondria metabolism and oxidative stress (Hatch, 1998; Ojcius et al, 1998). In cells exposed to oxidative stress down regulation of PI3K/Akt pathway results in high level of apoptosis (Taylor et al, 2005) and interestingly the oxidants stimulate Akt survival pathway (Klotz et al, 2000; Zhuang & Kochevar, 2003). Mechanical stress caused by growing inclusion could also induce phosphorylation of Akt in various cell types (Dimmeler et al, 1998; Kippenberger et al, 2005). Thus it is very well possible that Sn secretes effective proteins or the mechanical stress developed due to the development of inclusion could lead to this efficient survival signal, the necessity of which is evident from the fact that the treatment of Akt inhibitors in Sn infected cells leads to its sensitization.

4.7. NF- κ B is activated upon Sn infection

The nuclear factor- κ B family of transcription factors plays a central role in the host response to infection by microbial pathogens by orchestrating the innate and acquired host immune responses. Diverse signaling pathways that originate from many different cellular receptors and sensors activate the NF- κ B proteins. Many successful pathogens have acquired sophisticated mechanism to regulate this pathway by deploying subversive proteins or hijacking the host-signaling molecule. As cellular immune receptors like Toll Like Receptor (TLRs), cytokine receptors and TNFRs signals via NF- κ B after recognizing a variety of pathogen associated molecular patterns (PAMPs). Activation of NF- κ B following infection is reported in various pathogens. NF- κ B activation leads to the secretion of cytokines and chemokines, as a part of host defense response to trigger host innate immune response. On the other

hand the anti-apoptotic effect of NF- κ B is thought to be beneficial for intracellular pathogen that depends on host cell survival (Wan & Lenardo, 2010).

In Sn, biphasic activation of NF- κ B could be observed, early phase of infection, shortly after adhesion of the bacteria a transient translocation of the p65 component of NF- κ B could be observed (data not shown). It is very likely that this first wave of transient activation is via TLR signaling. At a later time point an unknown factor that depends on bacterial replication induces continuous localization of p65 and permanent degradation or ubiquitination of I κ B as well as the up-regulation of various anti-apoptotic genes. Hence, as discussed above this time resolved activation provides insight into two opposing effects of NF- κ B activation, initially beneficial for the host via activation of innate immune response and later advantageous for the pathogen, likely being casually involved in anti-apoptotic host cell phenotype. This second wave of activation persisted for a longer time of 72h, atypical with normal cells but a hallmark of certain cancers (Courtois & Smahi, 2006). An important feature associated with activation of NF- κ B is the anti-apoptotic phenotype which pathogens exploit to ensure the integrity of the infected cells. Sn infection promoted an up-regulation of cIAP1/2 and XIAP during the same time point as the NF- κ B activation. This supports how the pathogen benefits, particularly because unlike other intracellular pathogens Sn needs nearly 5 days or more to complete its life cycle.

Various pathogen factors have been reported for the NF- κ B regulation, like *sdbA* and *lubX* mutants failed to elicit constitutive NF- κ B activation and also exhibited severe growth defects in *L. pneumophila* (Bartfeld et al, 2009). Later the LegK1 protein was recognized as the direct activator of NF- κ B signaling. The pathogens

could target the host ubiquitinylation machinery, which plays a central role. Most of the effector proteins are primarily delivered through the type III secretion system as in *Yersinia* spp, or by type IV secretion system as in *Bartonella* spp. The YopJ/P protein of *Yersinia* block the NF- κ B pathway by blocking the pro-inflammatory cytokines, recognized later as cysteine proteases they also have a deubiquitylating and desumoylating activity, which prevents the ubiquitination of I κ B (Viboud & Bliska, 2005). In the case of *Salmonella* spp. AvrA and SseL inhibits deubiquitylation of I κ B. While the intracellular bacterial pathogen *Chlamydia trachomatis* inhibits NF- κ B translocation by Rel-A degradation by the *Chlamydia* specific proteases CT441 (Lad et al, 2007), and chlamydial protease-like activating factor (CPAF) (Christian et al, 2010). The chlamydial deubiquitylase and deneddylase (ChlADub) binds to I κ B and prevents its degradation (Le Negrate et al, 2008). While *Chlamydia pneumoniae*, which lacks ChlADub, uses an inclusion specific protein encoded by the locus CP0236 to sequester NF- κ B activator, ACT1/CIKS, which regulate NF- κ B (Wolf et al, 2009). In Sn infection as the second wave of activation persist for a longer time it is very likely that an unknown bacterial protein is playing a crucial role. More interestingly, the NF- κ B mutant cells showed a reduced infectivity of Sn as shown in the results. This indicates that some critical survival factor depending on NF- κ B is necessary for Sn survival or that NF- κ B regulates some cell surface receptors required for bacterial uptake.

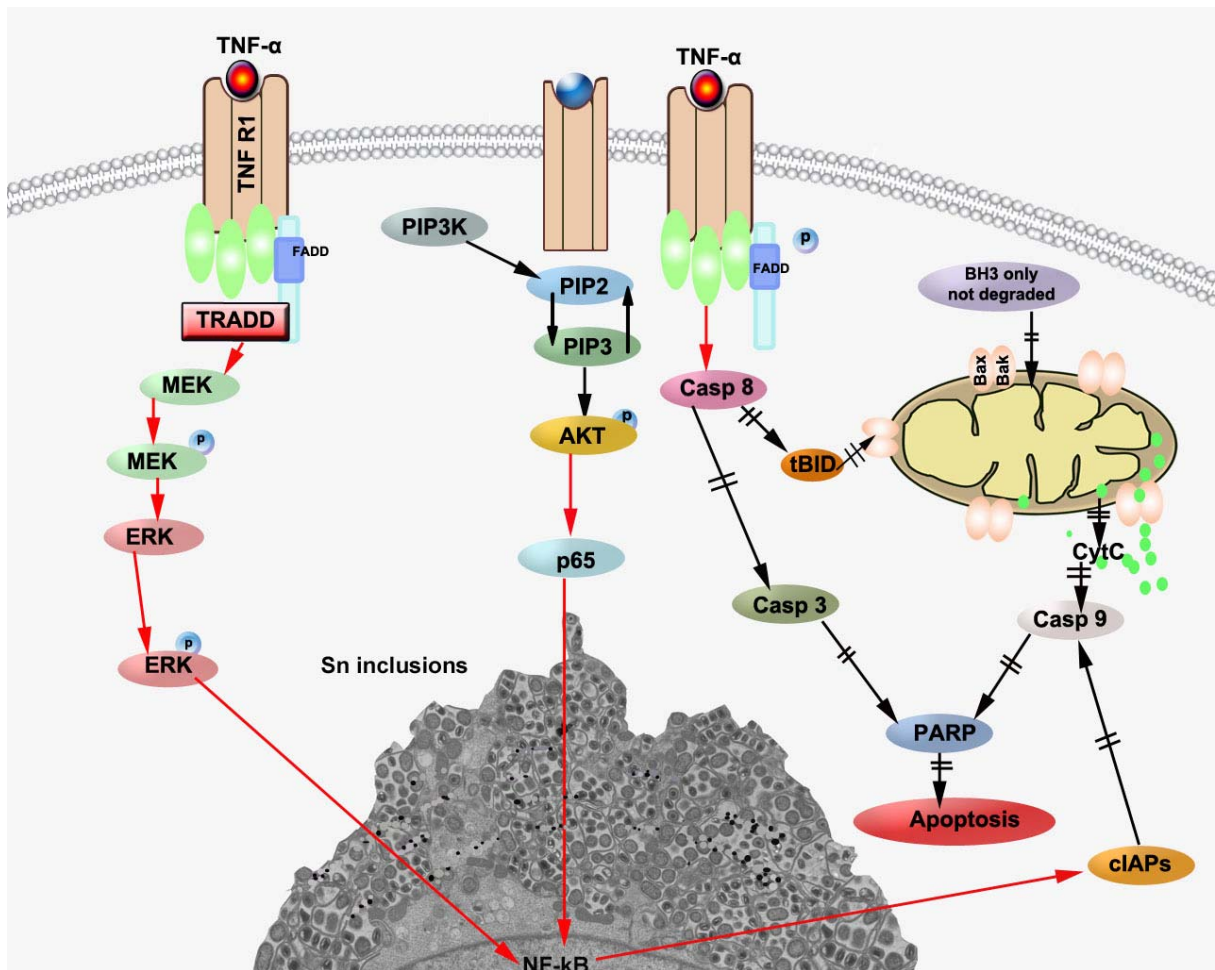


Figure 4.17. Overview of anti-apoptotic mechanisms in Sn infected cells: *Simkania* micro-manage the host signaling circuitry to favor the continued survival of the pathogen. Inhibition of apoptosis could be achieved by several different mechanisms. The various survival pathways activated by Sn is shown by red arrows and the pathways that they block to prevent apoptosis is shown by black arrows with cross bars. The black arrows with no bars indicate the possible upstream signals that promote the survival signals in Sn-infected cells. The Sn infection activates survival signal Akt upon infection, which could lead to the activation of NF- κ B. This could activate increased transcription of anti-apoptotic genes like IAPs. IAPs prevent the activation of caspases. Although the BH3 only proteins are not degraded upon infection, Sn prevents cytochrome c release from the infected cells which hinders the downstream activation of caspase-9 and effector caspase-3. Sn infection can also activate caspase-8 but do not activate the Bid cleavage and activation thereby protecting the mitochondria.

The figure 3.16 depicts the overall anti-apoptotic and survival signals generated upon Sn infection in cells. The survival signals are persistent throughout the infection. This raises the questions how these long-term signaling events are fueled even several days after the first interaction of the pathogen with the host cell. One could speculate that the bacterial factors play a crucial role in manipulating the host. Like other pathogenic members of the *Chlamydiales*, *Simkania* has a type III secretion system that may help to transport proteins across the inclusion membrane into the cytosol of the host. Secreted bacterial proteins may take over the pacemaker function in maintaining the host cell in a survival mode to guarantee such a long-term host-pathogen relation.

5. Outlook

The present study was an attempt to investigate on the evolutionary conservation of cell death modulation in the *Chlamydiales*. The newly discovered member of *Chlamydiales*, *Simkania negevensis* was under study. Since this pathogen differ from other *Chlamydiales* in their time span to complete the life cycle, it was obviously interesting to find the survival signals that would play a role. The experiments in this direction revealed that the mechanism of cell death inhibition is highly conserved in the order *Chlamydiales*, but still differ from the other members. Meanwhile, the differential activation of caspases should be given special attention, as the activated caspases in Sn infected cell could reveal more about pathogenesis and autophagy during infection. It is indicated in this work that activates PI3 kinase could lead to persistent NF- κ B activation, hence this needs further elucidation. It will be also interesting to investigate the possibility that strong and rather persistent activation of NF- κ B could promote development of cancer. One another interesting fact that came across was the reduced infectivity in NF- κ B mutant cells, investigation in this direction could reveal the factors that could be necessary for the survival or uptake of the bacteria. Special attention should be given to the yet to be published finding that, Sn resides in the endoplasmic reticulum (results from Dr. Mehlitz) unlike other *Chlamydiales*. This tempts one to think the mechanism that this pathogen would adapt to secrete its effector proteins across multi membranes. It would also be interesting to understand how this pathogen prevents endoplasmic reticulum stress induced cell death. Further studies on amoebae would reveal how this pathogen adapted itself for an obligate intracellular lifestyle and moreover, studies on

Dictyostelium discoideum, which could serve as a suitable model organism would reveal more hints on apoptosis, phagocytosis, endocytosis, membrane trafficking, vesicle sorting and pathogenesis.

More than anything the effector proteins that might imitate anti apoptotic host proteins and the one that play a role in maintaining the pathogen as a native component in the cell is yet to be discovered. This study could be further expanded to mouse models, which could reveal how severe could be an acute infection; this could also answer how Sn remained as an emerging pathogen. A closer look into pathogen clearance would be interesting. Since Sn and Cpn are known to occupy the same niche, it would be interesting to see how co-infection works. How the presence and development of one pathogen affects the other? Is there a mechanism of niche protection by these pathogens? Sn transcriptomics and metabolomics could also pave the way to find more interesting candidates that could play role in survival of the pathogen.

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7.1. Curriculum Vitaé

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Academic Qualification:

Degree/Award	Year	Institution & Board /University	Major Subjects	Result
Bachelor of Science (Agriculture)	2000 - 2004	GKVK, University of Agricultural Sciences (UAS) , Bangalore, INDIA	Agricultural Sciences	82%
Master of Science (Agricultural Biotechnology)	2004 - 2006	Kerala Agricultural University (KAU), Trivandrum, Kerala INDIA	Biotechnology	92%
Graduate Fellowship	May 2007 till date	Graduate School of Life Science, University of Wuerzburg,	Infection Biology, Cell Biology	-

Research Experience:

1) Year : 2004-2007

Institute : Department of Plant Biotechnology, College of Agriculture, Kerala Agricultural University, Trivandrum, Kerala, INDIA.

Master Thesis : '*Agrobacterium Tumefaciens* mediated genetic transformation in *Dendrobium* variety sonia 17 with 1-aminocyclopropane-1-carboxylic acid (ACC) antisense gene.'

2) Year : May 2007 - till date.

Institute : Theoder- Boveri Institute, Department of Microbiology, Biocentre, Am Hubland, Wuerzburg, Germany

Ph.D Thesis : 'Mechanisms of apoptosis regulation in human cells infected with *Simkania negevensis*'
Under Prof. Dr. Thomas Rudel,
Lehrstuhl für Mikobiologie, University of Wuerzburg, Germany

Awards and fellowships received:

- 1) 2000-2004 : All India Scholarship under ICAR (Indian Council of Agricultural Research) For Bachelors in Agriculture (Rank 612)
- 2) 2004-2006 : All India Scholarship under ICAR (Indian Council of Agricultural Research) For Masters in Agricultural Biotechnology (Rank 52)
- 3) 2004-2006 : KAU Award for Masters from the Kerala Agricultural University
- 4) 2006 : Indira Gandhi Post Graduate Scholarship, Govt. of India.
- 5) 2007-2010 : The Graduate School of Life Sciences (GSLS) fellowship by The Excellent Initiative of the German Federal and State Government, (Deutsche Forschungsgemeinschaft-DFG)

Oral presentations and posters accepted:

Karunakaran K. Oral presentation on 'Edible Vaccines' on the theme Sustainable Agriculture as a part of 'Prithvi' 2005 International Global Eco Meet, 21st Feb, 2005, Trivandrum, INDIA.

Karunakaran K, Mehlitz A and Rudel T poster on 'The pathogenic mechanisms of an emerging pathogen *Simkania Negevensis*' 2009 meeting on Microbial Pathogenesis and Host Cell Response at Cold Spring Harbor Laboratory, New York, USA.

Karunakaran K, Mehlitz A and Rudel T Oral presentation on 'Evolutionary conservation of infection-induced cell death inhibition among *Chlamydiales*'. 2010. 10th International conference on molecular epidemiology and evolutionary genetics of infectious diseases, Amsterdam, Netherlands.

Karunakaran K, Mehlitz A and Rudel T poster presentation on 'Evolutionary conservation of infection-induced cell death inhibition among *Chlamydiales*'. 2011 FEMS- Leopoldina- Symposium on Emerging topics in Microbial pathogenesis, würzburg, Germany.

Conferences and symposia attended:

- 1) ICAR National Symposium on Biotechnological Intervention for Improvement of Horticultural Crops: Issues and Strategies, organized by ICAR on 10 -12 Jan, 2005, Trissur, INDIA
- 2) Fellow Retreat of the Graduate School of Life Science, organized by the University of Wuerzburg at Schloss Zeitlitzheim, 27-29 June 2008, Wuerzburg, Germany
- 3) Third International Symposium organized by the Graduate School of Life Sciences University of Wuerzburg, 8 October 2008, Wuerzburg, Germany
- 4) Course on European Credit Transfer system Grundstufe 1 from the Zentrum für Sprachen und Mediendidaktik at the University of Wuerzburg, 21 June 2007, Wuerzburg, Germany
- 5) Workshop on "Presentation Technique" conducted by the Graduate School of Life sciences on 4-5 December 2007, Wuerzburg, Germany
- 6) Course on "Patent law in Life sciences" conducted by the GSLS, University of Wuerzburg on 30 June 2009, Wuerzburg, Germany
- 7) A seminar lecture on the "GxP- A Basic Introduction" conducted by Dr. J. Fensterle of Aeterna Zentaris GmbH, Wuerzburg, Germany
- 8) Leopoldina symposium on Leopoldina- Symposium on Emerging topics in Microbial pathogenesis, würzburg, Germany.
- 9) Deutcher Chlamydia workshop 2012 at Erfurt, Germany.

7.2. List of publications

1. **Karunakaran K**, Mehlitz A, Rudel T. Evolutionary conservation of infection-induced cell death inhibition among *Chlamydiales*. PLoS One. 2011 July; 6(7):e22528.
2. Sharma M, Machuy N, Böhme L, **Karunakaran K**, Mäurer AP, Meyer TF, Rudel T. HIF-1 α is involved in mediating apoptosis resistance to *Chlamydia trachomatis*-infected cells. Cell Microbiol. 2011 Oct; 13(10): 1573-85.
3. Mehlitz A, V kozjak-pavlovic, Huber A, **Karunakaran K**, Krohne G, Rudel T. *Simkania negevensis* requires mitofusin-2 for replication in the endoplasmic reticulum. (Manuscript in preparation).
4. Mehlitz A, Banhart S, Thorn H, **Karunakaran K**, Rudel T, Meyer TF. *Chlamydia trachomatis* L2 Tarp regulates immune signaling and survival in epithelial cells via PLCG in a serotype-specific manner. (Manuscript in preparation).